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(54) Title: VAULT AND VAULT-LIKE CARRIER MOLECULES

(57) Abstract: A method of using vaults as carrier molecules to deliver one or more than one substance to an organism, or to a specific tissue or to specific cells, or to an environmental medium. A vault-like particle. A method of preventing damage by one or more than one substance to an organism, to a specific tissue, to specific cells, or to an environmental medium, by sequestering the one or more than one substance within a vault-like particle. A method of delivering one or more than one substance or a sensor to an organism, to a specific tissue, to specific cells, or to an environmental medium. According to another embodiment of the present invention, there is provided a method of making vault-like particles, and making vault-like particles comprising one or more than one substance, or one or more than one sensor.

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10/547530**VAULT AND VAULT-LIKE CARRIER MOLECULES****CROSS-REFERENCE TO RELATED APPLICATION**

The present Application claims the benefit of United States provisional patent application 60/453,800 titled "Vault Nano Capsules," and filed March 10, 2003, the contents of which are incorporated in this disclosure by reference in their entirety.

**STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR
DEVELOPMENT**

This invention was made with United States Government support under National Science Foundation, Nano Science Interdisciplinary Research Team Grant No. MCB-0210690 National Science Foundation Grant No. MCB-9722353. The United States Government has certain rights in this invention.

BACKGROUND

Vaults are ubiquitous, highly conserved cellular components found in phylogeny as diverse as mammals, avians, amphibians, the slime mold *Dictyostelium discoideum*, and the protozoan *Trypanosoma brucei*. Scanning transmission electron microscopic analysis has shown that the molecular mass of vaults is about 12.9 ± 1 MDa, and cryo-electronmicrograph single particle reconstruction has determined that vaults have an overall dimension of about $420 \times 420 \times 750$ Å. Thus, vaults have a greater mass and size than many icosahedral viruses. The function of vaults is currently unknown.

Vaults are ribonucleoprotein particles comprising three different proteins, designated MVP, VPARP and TEP1, and between one and three different untranslated RNA molecules, designated vRNAs. For example, the rat *Rattus norvegicus* has only one form of vRNA per vault, while humans have three forms of vRNA per vault. The major vault protein, MVP, a 95.8 kDa protein in *Rattus norvegicus* and a 99.3 kDa protein in humans, is present in 96 copies per vault and accounts for about 75% of the total protein mass of the vault particle. The two other proteins, the vault poly-ADP ribose polymerase, VPARP, a 193.3 kDa protein in humans, and the telomerase/vault associated protein 1, TEP1, a 292 kDa protein in *Rattus norvegicus* and a 290 kDa protein in humans, are each present in between about 2 and 16 copies per vault.

VPARP, is a poly ADP-ribosyl polymerase apparently unique to vaults. It includes a region of about 350 amino acids that shares 28% identity with the catalytic domain of poly

ADP-ribosyl polymerase, PARP, a nuclear protein that catalyzes the formation of ADP-ribose polymers in response to DNA damage. VPARP catalyzes an NAD-dependent poly ADP-ribosylation reaction, and purified vaults have poly ADP-ribosylation activity that targets MVP, as well as VPARP itself.

5 Cryo-electron microscopy studies have determined that the vaults are hollow, barrel-like structures with two protruding end caps and an invaginated waist. Regular small openings surround the vault cap. These openings are large enough to allow small molecules and ions to enter the interior of the vault. The volume of the internal cavity of the vault is about $5 \times 10^7 \text{ \AA}^3$, large enough to enclose two ribosomes.

SUMMARY

10 According to one embodiment of the present invention, there is provided a method of using vaults as carrier molecules to deliver one or more than one substance to an organism, or to a specific tissue or to specific cells, or to an environmental medium. The method comprises providing vaults, incorporating the one or more than one substance into the vaults,
15 and administering the vaults comprising the one or more than one substance to the organism, to the specific tissue, to the specific cells, or to the environmental medium. In one embodiment, the vaults provided are purified from natural sources. In another embodiment, the vaults provided are generated using recombinant technology. In one embodiment, incorporation is accomplished by incubating the vaults with the one or more than one
20 substance. In one embodiment, the one or more than one substance is selected from the group consisting of an enzyme, a pharmaceutical agent, a plasmid, a polynucleotide, a polypeptide, a sensor and a combination of the preceding.

According to another embodiment of the present invention, there is provided a vault-like particle comprising MVP. In one embodiment, the vault-like particle further comprises
25 VPARP or modified VPARP, or a portion of VPARP or a modified portion of VPARP. In another embodiment, the vault-like further comprises TEP1 or modified TEP1, or a portion of TEP1 or a modified portion of TEP1.

According to another embodiment of the present invention, there is provided a vault-like particle comprising modified MVP. In one embodiment, the modified MVP comprises
30 an amino acid sequence added to the N-terminal of the MVP which results in one or more than one substance-binding domain within the vault-like particle. In another embodiment, the one or more than one substance-binding domain is between 1 and 95 substance-binding

domains. In another embodiment, the one or more than one substance-binding domain is 96 substance-binding domains. In another embodiment, the one or more than one substance-binding domain is greater than 96 substance-binding domains. In one embodiment, the one or more than one substance-binding domain within the vault-like particle is one or more than one heavy metal binding domain. In a preferred embodiment, the one or more than one heavy metal binding domain binds a heavy metal selected from the group consisting of cadmium, copper, gold and mercury. In a preferred embodiment, the peptide added to the N-terminal is a cysteine-rich peptide. In a preferred embodiment, the one or more than one substance-binding domain within the vault-like particle is one or more than one polynucleotide-binding domain. In a preferred embodiment, the one or more than one polynucleotide-binding domain is a non-specific polynucleotide-binding peptide. In a preferred embodiment, the one or more than one polynucleotide-binding domain is a specific polynucleotide-binding peptide.

In another embodiment, the modified MVP of the vault-like particle comprising modified MVP comprises an amino acid sequence added to the N-terminal of the MVP creates a sensor in the vault-like particle. In one embodiment, the sensor is selected from the group consisting of a chemical sensor, an ionic sensor, a microorganism sensor, an optical sensor and a pH sensor. In one embodiment, the sensor is a green fluorescent protein.

In another embodiment, the modified MVP of the vault-like particle comprising modified MVP comprises an amino acid sequence added to the C-terminal of the MVP which results in one or more than one receptor-binding domain. In one embodiment, the one or more than one receptor-binding domain is between 1 and 95 receptor-binding domains. In another embodiment, the one or more than one receptor-binding domain is 96 receptor-binding domains. In another embodiment, the one or more than one receptor-binding domain is greater than 96 receptor-binding domains. In one embodiment, the one or more than one receptor-binding domain is non-specific. In another embodiment, the one or more than one receptor-binding domain is specific.

In another embodiment, the modified MVP further comprises an amino acid sequence added to the C-terminal of the MVP which results in one or more than one receptor-binding domain. In one embodiment, the one or more than one receptor-binding domain is between 1 and 95 receptor-binding domains. In another embodiment, the one or more than one receptor-binding domain is 96 receptor-binding domains. In another embodiment, the one or

more than one receptor-binding domain, is greater than 96 receptor-binding domains. In one embodiment, the one or more than one receptor-binding domain is non-specific. In another embodiment, the one or more than one receptor-binding domain is specific.

In another embodiment, the modified MVP comprises both an amino acid sequence
5 added to the C-terminal of the MVP and an amino acid sequence added to the N-terminal of the MVP.

According to another embodiment of the present invention, there is provided a vault-like particle comprising MVP or modified MVP, and further comprises VPARP or a portion of VPARP comprising at least about 150 consecutive residues of VPARP. In one
10 embodiment, the portion of VPARP comprises residues from about residue 1562 to 1724 of human VPARP, SEQ ID NO:3. In another embodiment, the portion of VPARP comprises residues from about residue 1473 to 1724 of human VPARP, SEQ ID NO:3. In another embodiment, the VPARP or portion of VPARP is modified. In one embodiment, the modification comprises adding an amino acid sequence added to the C-terminal of the
15 VPARP or portion of VPARP. In another embodiment, the modification comprises adding an amino acid sequence added to the N-terminal of the VPARP or portion of VPARP. In another embodiment, the modification comprises adding an amino acid sequence added to both the C-terminal and the N-terminal of the VPARP or portion of VPARP. In one embodiment, the modified MVP comprises an amino acid sequence added to the C-terminal
20 of the MVP. In another embodiment, the modified MVP comprises an amino acid sequence added to the N-terminal of the MVP. In another embodiment, the modified MVP comprises both a peptide added to the C-terminal and a peptide added to the N-terminal.

According to another embodiment of the present invention, there is provided a method of preventing damage by one or more than one substance to an organism, to a specific tissue,
25 to specific cells, or to an environmental medium, by sequestering the one or more than one substance within a vault-like particle. The method comprises providing vault-like particles, administering the vault-like particles to the organism, tissue, cells or environmental medium, and allowing the vault-like particles to sequester the one or more than one substance within the vault-like particles. In one embodiment, the one or more than one substance is a heavy
30 metal selected from the group consisting of cadmium, copper, gold and mercury. In another embodiment, the one or more than one substance is a toxin selected from the group consisting of arsenate, dioxin, an organochlorine, a pentachlorophenol and a polychlorinated biphenyl.

In one embodiment, providing the vault-like particles comprises expressing the vault-like particles in a eukaryotic organism.

According to another embodiment of the present invention, there is provided a method of delivering one or more than one substance to an organism, to a specific tissue, to specific
5 cells, or to an environmental medium. The method comprises providing vault-like particles comprising the one or more than one substance, and administering the vault-like particles comprising the one or more than one substance to the organism, tissue, cells or environmental medium. In one embodiment, the vault-like particles comprise, consist essentially of or consist of a modified MVP in addition to the one or more than one
10 substance. In another embodiment, the vault-like particles comprise a modified VPARP or modified portion of VPARP. In another embodiment, the vault-like particles comprise both a modified MVP according to the present invention, and a modified VPARP or modified portion of VPARP. In another embodiment, the one or more than one substance is selected from the group consisting of an enzyme, a pharmaceutical agent, a plasmid, a polynucleotide,
15 a polypeptide, a sensor and a combination of the preceding. In another embodiment, the one or more than one substance is adenosine deaminase.

According to another embodiment of the present invention, there is provided a method of delivering one or more than one sensor to an organism, to a specific tissue, to specific cells, or to an environmental medium. The method comprises providing a vault-like particle
20 comprising the one or more than one sensor and administering the vault-like particle to the organism, specific tissue, specific cells, or environmental medium. In one embodiment, the vault-like particles comprise, consist essentially of or consist of a modified MVP, in addition to the one or more than one sensor. In another embodiment, the vault-like particles comprise a modified VPARP or modified portion of VPARP. In another embodiment, the vault-like
25 particles comprise both a modified MVP, and a modified VPARP or modified portion of VPARP. In one embodiment, the sensor is selected from the group consisting of a chemical sensor, a fluorescent sensor, an ionic sensor, a microorganism sensor, an optical sensor, and a pH sensor.

According to another embodiment of the present invention, there is provided a method
30 of detecting a signal from a sensor within an organism, or a specific tissue or specific cells. The method comprises delivering one or more than one sensor to an organism, to a specific tissue, to specific cells, or to an environmental medium according to the present invention,

and detecting the presence of the sensor. In one embodiment, detection is accomplished by fluorometry or by spectrophotometry.

According to another embodiment of the present invention, there is provided a method of making vault-like particles. The method comprises creating polynucleotide sequences encoding one or more than one polypeptide selected from the group consisting of MVP, modified MVP, VPARP, a portion of VPARP, modified VPARP, a modified portion of VPARP, TEP1, a portion of TEP1, modified TEP1 and a modified portion of TEP1, using the polynucleotide sequences created to generate a bacmid DNA, using the bacmid DNA to generate a baculovirus comprising the sequence, and using the baculovirus to infect insect cells for protein production using an *in situ* assembly system.

According to another embodiment of the present invention, there is provided a method of making vault-like particles comprising one or more than one substance. The method comprises making vault-like particles according to claim 63, and co-incubated the vault-like particles with the one or more than one substance. In one embodiment, the one or more than one substance is selected from the group consisting of enzyme, a pharmaceutical agent, a plasmid, a polynucleotide, a polypeptide, a sensor and a combination of the preceding. In another embodiment, the method further comprises purifying the vault-like particles after making the vault-like particles.

DESCRIPTION

According to one embodiment of the present invention, there is provided a method of using vaults as carrier molecules to deliver one or more than one substance to an organism, or to a specific tissue or specific cells. The method comprises administering vaults comprising the substance to the organism, tissue or cells.

According to another embodiment of the present invention, there is provided a vault-like particle useful as a carrier molecule for delivering one or more than one substance to a living system, such as an organism, specific tissue or specific cell, or to an environmental medium. According to another embodiment of the present invention, there is provided a method of delivering one or more than one substance to an organism, or to a specific tissue or specific cells, or to an environmental medium. The method comprises providing vault-like particles comprising the substance, and administering the vault-like particles comprising the substance to the organism, tissue or cells, or to the environmental medium.

According to another embodiment of the present invention, there is provided a method

of delivering vault-like particles to a specific tissue or specific cells, or to an environmental medium. The method comprises providing vault-like particles having a receptor-binding domain on the surface of the vault-like particles, and administering the vault-like particles to the tissue or cells, or to the environmental medium.

5 According to another embodiment of the present invention, there is provided a vault-like particle useful for sequestering the one or more than one substance within the vault-like particle. According to another embodiment of the present invention, there is provided a method of preventing damage by one or more than one substance to an organism, or to a specific tissue or specific cells, or to an environmental medium, by sequestering the one or
10 more than one substance within a vault-like particle. The method comprises providing vault-like particles comprising one or more than one substance-binding domain within the vault-like particle, administering the vault-like particles to the organism, tissue or cells, or to the environmental medium, and allowing the vault-like particles to sequester the one or more than one substance within the vault-like particles.

15 Advantageously, both vaults and vault-like particles are resistant to degradation, such as intracellular degradation or environmental degradation, and therefore, can be used to deliver substances to or to remove substances from both living and non-living systems. The embodiments of the present invention will now be disclosed in greater detail.

As used in this disclosure, "MVP," "VPARP" and "TEP1" means the full naturally
20 occurring polypeptide sequence. "vRNA" means the full naturally occurring polynucleotide sequence. As will be appreciated by one of ordinary skill in the art with reference to this disclosure, the actual sequence of any of MVP, VPARP, TEP1 and vRNAs can be from any species suitable for the purposes disclosed in this disclosure, even though reference or examples are made to sequences from specific species. For example, when delivering
25 substances to human organs or tissues, it is preferred to use human vaults or vault-like particles comprising human sequences for MVP, VPARP, TEP1 and vRNAs. Further, as will be appreciated by one of ordinary skill in the art with reference to this disclosure, there are some intraspecies variations in the sequences of MVP, VPARP, TEP1 and vRNAs that are not relevant to the purposes of the present invention. Therefore, references to MVP,
30 VPARP, TEP1 and vRNAs are intended to include such intraspecies variants.

As used in this disclosure, the term "vault" or "vault particle," as compared to the term "vault-like particle" defined below, refers to a naturally occurring macro-molecular

structure having MVP, VPARP, TEP1 and one or more than one vRNA, whether purified from natural sources or generated through recombinant technology.

As used in this disclosure, the term "vault-like particle" refers to a macro-molecular structure comprising any of the following:

- 5 1) MVP without VPARP, TEP1 and vRNA;
- 2) MVP and either VPARP or a portion of VPARP, without TEP1 and vRNA;
- 3) MVP and TEP1 or a portion of TEP1 with or without the one or more than one vRNA, and without VPARP;
- 4) MVP without VPARP, TEP1 and vRNA, where the MVP is modified to attract a specific substance within the vault-like particle, or modified to attract the vault-like particle to a specific tissue, cell type or environmental medium, or modified both to attract a specific substance within the vault-like particle and to attract the vault particle to a specific tissue, cell type or environmental medium; and
- 10 5) MVP, and either VPARP or a portion of VPARP, or TEP1 or a portion of TEP1 with or without the one or more than one vRNA, or with both VPARP or a portion of VPARP, and TEP1, with or without the one or more than one vRNA, where one or more than one of the MVP, VPARP or portion of VPARP and TEP1 is modified to attract a specific substance within the vault-like particle, or modified to attract the vault particle to a specific tissue, cell type or environmental medium, or modified both to attract a specific substance within the vault-like particle and to attract the vault particle to a specific tissue, cell type or
- 15 20 environmental medium.

As used in this disclosure, the term "modified" and variations of the term, such as "modification," means one or more than one change to the naturally occurring sequence of MVP, VPARP or TEP1 selected from the group consisting of addition of a polypeptide sequence to the C-terminal, addition of a polypeptide sequence to the N-terminal, deletion of between about 1 and 100 amino acid residues from the C-terminal, deletion of between about 1 and 100 amino acid residues from the N-terminal, substitution of one or more than one amino acid residue that does not change the function of the polypeptide, as will be appreciated by one of ordinary skill in the art with reference to this disclosure, such as for

25 30 example, an alanine to glycine substitution, and a combination of the preceding.

As used in this disclosure, the term "human" means "*Homo sapiens*."

As used in this disclosure, the terms "organism," "tissue" and "cell" include

naturally occurring organisms, tissues and cells, genetically modified organisms, tissues and cells, and pathological tissues and cells, such as tumor cell lines *in vitro* and tumors *in vivo*.

As used in this disclosure, the term "environmental medium" means a non-living composition, composite, material, or mixture.

5 As used in this disclosure, the term "administering" includes any suitable route of administration, as will be appreciated by one of ordinary skill in the art with reference to this disclosure, including direct injection into a solid organ, direct injection into a cell mass such as a tumor, inhalation, intraperitoneal injection, intravenous injection, topical application on a mucous membrane, or application to or dispersion within an environmental medium, and a
10 combination of the preceding. In one embodiment, the dosage of vaults or vault-like particles, with or without one or more than one substance enclosed within the vaults or vault-like particles, is between about 0.1 and 10,000 micrograms per kilogram of body weight or environmental medium. In another embodiment, the dosage of vaults or vault-like particles, with or without one or more than one substance enclosed within the vaults or vault-like
15 particles, is between about 1 and 1,000 micrograms per kilogram of body weight or environmental medium. In another embodiment, the dosage of vaults or vault-like particles, with or without one or more than one substance enclosed within the vaults or vault-like particles, is between about 10 and 1,000 micrograms per kilogram of body weight or environmental medium. For intravenous injection and intraperitoneal injection, the dosage is
20 preferably administered in a final volume of between about 0.1 and 10 ml. For inhalation the dosage is preferably administered in a final volume of between about 0.01 and 1 ml. As will be appreciated by one of ordinary skill in the art with reference to this disclosure, the dose can be repeated a one or more than one of times as needed using the same parameters to effect the purposes disclosed in this disclosure.

25 As used in this disclosure, "MS2" means the Enterobacteriophage MS2 coat protein, which is an RNA-binding protein that specifically binds a 21-nt RNA stem-loop with high affinity.

 As used in this disclosure, the term "comprise" and variations of the term, such as "comprising" and "comprises," are not intended to exclude other additives, components,
30 integers or steps.

 In one embodiment, the present invention is a method of using naturally occurring vaults as carrier molecules to deliver one or more than one substance to an organism, or to a

specific tissue or specific cells, or to an environmental medium. The method comprises, first, providing vaults. In one embodiment, the vaults are purified from natural sources, such as mammalian liver or spleen tissue, using methods known to those with skill in the art, such as for example tissue homogenization, differential centrifugation, discontinuous sucrose gradient fractionation and cesium chloride gradient fractionation. In another embodiment, 5 the vaults are made using recombinant technology. Next, the one or more than one substance is incorporated into the provided vaults. In a preferred embodiment, incorporation is accomplished by incubating the vaults with the one or more than one substance at an appropriate temperature and for an appropriate time, as will be appreciated by one of 10 ordinary skill in the art with reference to this disclosure. The vaults containing the one or more than one substance are then purified, such as for example sucrose gradient fractionation, as will be appreciated by one of ordinary skill in the art with reference to this disclosure. In a preferred embodiment, the one or more than one substance is selected from 15 the group consisting of an enzyme, a pharmaceutical agent, a plasmid, a polynucleotide, a polypeptide, a sensor and a combination of the preceding. Next, the vaults comprising the one or more than one substance are administered to an organism, to a specific tissue, to specific cells, or to an environmental medium. Administration is accomplished using any suitable route, as will be appreciated by one of ordinary skill in the art with reference to this disclosure.

20 According to another embodiment of the present invention, there is provided a vault-like particle useful as a carrier molecule for delivering one or more than one substance to an organism, to a specific tissue, to specific cells, or to an environmental medium, or useful for preventing damage by one or more than one substance to an organism, to a specific tissue, to specific cells, or to an environmental medium, by sequestering the one or more than one 25 substance within a vault-like particle. The vault-like particle comprises MVP or modified MVP, and can further comprise VPARP or modified VPARP, a portion of VPARP or a modified portion of VPARP, and TEP1 or modified TEP1, a portion of TEP1 or a modified portion of TEP1 with or without the one or more than one vRNA. In a preferred embodiment, the modifications are designed to attract a specific substance within the vault- 30 like particle, to attract the vault-like particle to a specific tissue or cell type, or both to attract a specific substance within the vault-like particle and to attract the vault particle to a specific tissue or cell type.

In one embodiment, the MVP is human MVP, SEQ ID NO:1, GenBank accession number CAA56256, encoded by the cDNA, SEQ ID NO:2, GenBank accession number X79882. In another embodiment, the VPARP is human VPARP, SEQ ID NO:3, GenBank accession number AAD47250, encoded by the cDNA, SEQ ID NO:4, GenBank accession number AF158255. In another embodiment, the TEP1 is human TEP1, SEQ ID NO:5, GenBank accession number AAC51107, encoded by the cDNA, SEQ ID NO:6, GenBank accession number U86136. In another embodiment, the vRNA is human vRNA, SEQ ID NO:7, GenBank accession number AF045143, SEQ ID NO:8, GenBank accession number AF045144, or SEQ ID NO:9, GenBank accession number AF045145, or a combination of the preceding.

In one embodiment, the MVP is *Rattus norvegicus* MVP, SEQ ID NO:10, GenBank accession number AAC52161, encoded by the cDNA, SEQ ID NO:11, GenBank accession number U09870. In another embodiment, the TEP1 is *Rattus norvegicus* TEP1, SEQ ID NO:12, GenBank accession number AAB51690, encoded by the cDNA, SEQ ID NO:13, GenBank accession number U89282. In another embodiment, the vRNA is *Rattus norvegicus* vRNA, SEQ ID NO:14, GenBank accession number Z1171. As can be seen, *Rattus norvegicus* MVP and human MVP share over 90% homology.

The following disclosure of vault protein modifications references specific examples using specific human and *Rattus norvegicus* sequences of MVP, VPARP and TEP1 sequences, however, as will be appreciated by one of ordinary skill in the art with reference to this disclosure, corresponding modifications can be made using other sequences of these species and can be made using sequences from other species as appropriate for the disclosed purposes.

According to one embodiment of the present invention, there is provided a vault-like particle comprising, consisting essentially of, or consisting of modified MVP. In a preferred embodiment, the modification comprises adding an amino acid sequence to the N-terminal of the MVP which results in one or more than one substance-binding domain within the vault-like particle. When each copy of the MVP is modified in this manner, one or more than one of the substance-binding domains, such as 96 substance-binding domains, is present in each vault-like particle, however, vault-like particles can also be assembled from a mixture of MVP with the N-terminal modified and MVP without the N-terminal modified, to create vault-like particle with less than 96 substance-binding domains in the vault-like particle, and

the added amino acid terminal sequences can be polymerized as will be appreciated by one of ordinary skill in the art with reference to this disclosure to create more than 96 substance-binding domains in the vault-like particle.

In a preferred embodiment, there is provided a vault-like particle comprising,
5 consisting essentially of, or consisting of an MVP modified by adding a peptide to the N-terminal to create a one or more than one of heavy metal binding domains. In a preferred embodiment, the heavy metal binding domains bind a heavy metal selected from the group consisting of cadmium, copper, gold and mercury. In a preferred embodiment, the peptide added to the N-terminal is a cysteine-rich peptide (CP), such as for example, SEQ ID NO:15,
10 the MVP is human MVP, SEQ ID NO:1, and the modification results in CP-MVP, SEQ ID NO:16, encoded by the cDNA, SEQ ID NO:17. In another preferred embodiment, the cysteine-rich peptide is SEQ ID NO:15, the MVP is *Rattus norvegicus* MVP, SEQ ID NO:10, and the modification results in CP-MVP, SEQ ID NO:18, encoded by the cDNA, SEQ ID NO:19. These embodiments are particularly useful because vault-like particles
15 consisting of CP-MVP, SEQ ID NO:16 or SEQ ID NO:18, are stable without the presence of other vault proteins.

In another embodiment, there is provided a vault-like particle comprising, consisting essentially of, or consisting of an MVP modified by adding a peptide to the N-terminal to create one or more than one polynucleotide-binding domain. In a preferred embodiment, the
20 peptide is a non-specific polynucleotide-binding peptide, such as for example, HisT7, SEQ ID NO:20, encoded by the cDNA, SEQ ID NO:21, or a polylysine such as SEQ ID NO:22, encoded by the cDNA, SEQ ID NO:23, the MVP is human MVP, SEQ ID NO:1, and the modification results in HisT7-MVP, SEQ ID NO:24, encoded by the cDNA, SEQ ID NO:25, or in polylysine-MVP, SEQ ID NO:26, encoded by the cDNA, SEQ ID NO:27, respectfully.
25 In another preferred embodiment, the peptide is a non-specific polynucleotide-binding peptide, such as for example, HisT7, SEQ ID NO:20, encoded by the cDNA, SEQ ID NO:21, or a polylysine such as SEQ ID NO:22, encoded by the cDNA, SEQ ID NO:23, the MVP is *Rattus norvegicus* MVP, SEQ ID NO:10, and the modification results in HisT7-MVP, SEQ ID NO:28, encoded by the cDNA, SEQ ID NO:29, or in polylysine-MVP, SEQ
30 ID NO:30, encoded by the cDNA, SEQ ID NO:31, respectfully. HisT7-MVP, SEQ ID NO:24 and SEQ ID NO:28, are examples of modified MVP that can also be used to bind specific antibodies within the vault-like particle, in these cases, the T7 monoclonal antibody,

but corresponding modifications can be made to bind other specific antibodies, as will be appreciated by one of ordinary skill in the art with reference to this disclosure. In another preferred embodiment, the peptide is a specific DNA binding peptide, such as for example, GAL4, SEQ ID NO:32, encoded by the cDNA, SEQ ID NO:33, the MVP is human MVP, SEQ ID NO:1, and the modification results in GAL4-MVP, SEQ ID NO:34, encoded by the cDNA, SEQ ID NO:35. In another preferred embodiment, the peptide is a specific DNA binding peptide, such as for example, GAL4, SEQ ID NO:32, encoded by the cDNA, SEQ ID NO:33, the MVP is *Rattus norvegicus* MVP, SEQ ID NO:10, and the modification results in GAL4-MVP, SEQ ID NO:36, encoded by the cDNA, SEQ ID NO:37. In another preferred embodiment, the peptide is a specific RNA binding peptide, such as for example, MS2, SEQ ID NO:38, encoded by the cDNA, SEQ ID NO:39, the MVP is human MVP, SEQ ID NO:1, and the modification results in MS2-MVP, SEQ ID NO:40, encoded by the cDNA, SEQ ID NO:41. In another preferred embodiment, the peptide is an RNA binding peptide, such as for example, MS2, SEQ ID NO:38, encoded by the cDNA, SEQ ID NO:39, the MVP is *Rattus norvegicus* MVP, SEQ ID NO:10, and the modification results in MS2-MVP, SEQ ID NO:42, encoded by the cDNA, SEQ ID NO:43.

In another embodiment, there is provided a vault-like particle comprising, consisting essentially of, or consisting of an MVP modified by adding a peptide to the N-terminal to create a sensor in the vault-like particle. The sensor can be any suitable sensor, as will be appreciated by one of ordinary skill in the art with reference to this disclosure, such as for example, a chemical sensor such as a cyclic-AMP binding protein, an ionic sensor such as a calcium or potassium sensor, a microorganism sensor such as an antibody specific for *E. coli*, an optical sensor such as a quantum dot, and a pH sensor such as green fluorescence protein. In a preferred embodiment, the sensor is a fluorescent protein, such as green fluorescent protein (GL), SEQ ID NO:44, encoded by the cDNA, SEQ ID NO:45, the MVP is human MVP, SEQ ID NO:1, and the modification results in GL-MVP, SEQ ID NO:46, encoded by the cDNA, SEQ ID NO:47. In another preferred embodiment, the sensor is a fluorescent protein, such as green fluorescent protein (GL), SEQ ID NO:44, encoded by the cDNA, SEQ ID NO:45, the MVP is *Rattus norvegicus* MVP, SEQ ID NO:10, and the modification results in GL-MVP, SEQ ID NO:48, encoded by the cDNA, SEQ ID NO:49.

In another embodiment, there is provided a vault-like particle comprising MVP or modified MVP, and further comprising VPARP or a portion of VPARP comprising at least

about 150 consecutive residues of VPARP, and modified by adding a peptide to either the C-terminal or the N-terminal to create a one or more than one of substance-binding domains or a one or more than one of sensors within the vault-like particles having the same purposes as disclosed with reference to modified MVP in this disclosure. By way of example only, in

5 one embodiment, the residues are from about residue 1562 to residue 1724 of human VPARP, SEQ ID NO:3. In another embodiment, the residues are from about residue 1473 to residue 1724 of human VPARP, SEQ ID NO:3. The substance-binding domains on the VPARP or portion of VPARP serve the same functions as disclosed in this disclosure with respect to N-terminal modifications of MVP. For example, in one embodiment, the vault-

10 like particles comprise residues 1473-1724 of VPARP, SEQ ID NO:3, modified by adding CP, SEQ ID NO:15, to the N-terminal, to create (1473-1724)CP-VPARP, SEQ ID NO:50, encoded by the cDNA, SEQ ID NO:51. In another embodiment, the vault-like particles comprise VPARP, SEQ ID NO:3, modified by adding CP, SEQ ID NO:15, to the N-terminal, to create CP-VPARP, SEQ ID NO:52, encoded by the cDNA, SEQ ID NO:53. In

15 one embodiment, the vault-like particles comprise residues 1473-1724 of VPARP, SEQ ID NO:3, modified by adding GAL4, SEQ ID NO:32, to the N-terminal, to create GAL4-(1473-1724)VPARP, SEQ ID NO:54, encoded by the cDNA, SEQ ID NO:55. In another embodiment, the vault-like particles comprise VPARP, SEQ ID NO:3, modified by adding GAL4, SEQ ID NO:32, to the N-terminal, to create GAL4-VPARP, SEQ ID NO:56,

20 encoded by the cDNA, SEQ ID NO:57. In another embodiment, the vault-like particles comprise residues 1473-1724 of VPARP, SEQ ID NO:3, modified by adding GL, SEQ ID NO:44, to the N-terminal, to create GL-(1473-1724)VPARP, SEQ ID NO:58, encoded by the cDNA, SEQ ID NO:59. In another embodiment, the vault-like particles comprise VPARP, SEQ ID NO:3, modified by adding GL, SEQ ID NO:44, to the N-terminal, to

25 create GL-VPARP, SEQ ID NO:60, encoded by the cDNA, SEQ ID NO:61. In another embodiment, the vault-like particles comprise residues 1473-1724 of VPARP, SEQ ID NO:3, modified by adding MS2, SEQ ID NO:38, to the N-terminal, to create MS2-(1473-1724)VPARP, SEQ ID NO:62, encoded by the cDNA, SEQ ID NO:63. In another embodiment, the vault-like particles comprise VPARP, SEQ ID NO:3, modified by adding

30 MS2, SEQ ID NO:38, to the N-terminal, to create MS2-VPARP, SEQ ID NO:64, encoded by the cDNA, SEQ ID NO:65. In another embodiment, the vault-like particles comprise residues 1473-1724 of VPARP, SEQ ID NO:3, modified by adding a *Photinus pyralis*

luciferase (LUC), SEQ ID NO:66 GenBank accession number P08659, encoded by the pGL3-Basic vector SEQ ID NO:67, GenBank accession number U47295 to the N-terminal, to create LUC-(1473-1724)VPARP, SEQ ID NO:68, encoded by the cDNA, SEQ ID NO:69. In another embodiment, the vault-like particles comprise VPARP, SEQ ID NO:3, modified by adding LUC, SEQ ID NO:66, to the N-terminal, to create LUC-VPARP, SEQ ID NO:71, encoded by the cDNA, SEQ ID NO:72. Further, as will be appreciated by one of ordinary skill in the art with reference to this disclosure, the present invention also includes corresponding modifications to the C-terminal of VPARP or a portion of VPARP, and serve the same function. In a preferred embodiment, the substance binding domain binds the enzyme adenosine deaminase.

According to one embodiment of the present invention, there is provided a vault-like particle comprising, consisting essentially of, or consisting of MVP modified by adding an amino acid sequence to the C-terminal of the MVP which results in one or more than one receptor-binding domain, such as a protein targeting domain, on the surface of the vault-like particle. When each copy of the MVP is modified in this manner, one or more than one of the receptor-binding domains, such as 96 receptor-binding domains, is present on each vault-like particle, however, vault-like particles can also be assembled from a mixture of MVP with the C-terminal modified and MVP without the C-terminal modified, to create vault-like particle with less than 96 receptor-binding domains on the vault-like particle.

In a preferred embodiment, there is provided a vault-like particle comprising, consisting essentially of, or consisting of an MVP modified by adding a peptide to the C-terminal to create a one or more than one of eukaryotic cell receptor-binding domains on the exterior of the vault-like particles. In a preferred embodiment, the eukaryotic cell receptor-binding domain is generally non-specific. For example, in one embodiment, the peptide is Antennapedia (ANT), SEQ ID NO:72, encoded by the cDNA, SEQ ID NO:73, the MVP is human MVP, SEQ ID NO:1, and the modification results in MVP-ANT, SEQ ID NO:74, encoded by the cDNA, SEQ ID NO:75. In another embodiment, the peptide is ANT, SEQ ID NO:72, encoded by the cDNA, SEQ ID NO:73, the MVP is *Rattus norvegicus* MVP, SEQ ID NO:10, and the modification results in MVP-ANT, SEQ ID NO:76, encoded by the cDNA, SEQ ID NO:77. In another embodiment, the peptide is HIV-Tat (TAT), SEQ ID NO:78, encoded by the cDNA, SEQ ID NO:79, the MVP is human MVP, SEQ ID NO:1, and the modification results in MVP-TAT, SEQ ID NO:80, encoded by the cDNA, SEQ ID

NO:81. In another embodiment, the peptide is TAT, SEQ ID NO:78, encoded by the cDNA, SEQ ID NO:79, the MVP is *Rattus norvegicus* MVP, SEQ ID NO:10, and the modification results in MVP-TAT, SEQ ID NO:82, encoded by the cDNA, SEQ ID NO:83. In another embodiment, the eukaryotic cell receptor-binding domain is specific to a certain type of eukaryotic cell receptor, such as for example a carcinoembryonic antigen receptor, a protein found on the surface of about 50% of all human tumors, or an epidermal growth factor (EGF) receptor. For example, in one embodiment, the peptide is anti-CEA scFv diabody (α CEA), SEQ ID NO:84, encoded by the cDNA, SEQ ID NO:85, the MVP is human MVP, SEQ ID NO:1, and the modification results in MVP- α CEA, SEQ ID NO:86, encoded by the cDNA, SEQ ID NO:87. In another embodiment, the peptide is α CEA, SEQ ID NO:84, encoded by the cDNA, SEQ ID NO:85, the MVP is *Rattus norvegicus* MVP, SEQ ID NO:10, and the modification results in MVP- α CEA, SEQ ID NO:88, encoded by the cDNA, SEQ ID NO:89. In another embodiment, the peptide is EGF, SEQ ID NO:90, encoded by the cDNA, SEQ ID NO:91, the MVP is human MVP, SEQ ID NO:1, and the modification results in MVP-EGF, SEQ ID NO:92, encoded by the cDNA, SEQ ID NO:93. In another embodiment, the peptide is EGF, SEQ ID NO:90, encoded by the cDNA, SEQ ID NO:91, the MVP is *Rattus norvegicus* MVP, SEQ ID NO:10, and the modification results in MVP-EGF, SEQ ID NO:94, encoded by the cDNA, SEQ ID NO:95.

According to one embodiment of the present invention, there is provided a vault-like particle comprising, consisting essentially of, or consisting of MVP modified by adding an amino acid sequence to the N-terminal and also modified by adding an amino acid sequence to the C-terminal. The modification of the N-terminal and the modification of the C-terminal can be any modification as disclosed in this disclosure, for the same purposes as disclosed in this disclosure. For example, the modification of the N-terminal can result in a substance-binding domain, such as for example a heavy metal binding domain or a polynucleotide binding domain, or can result in a sensor within the vault-like particle. The modification of the C-terminal can result in one or more than one receptor-binding domain on the surface of the vault-like particle. By way of example only, in one embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding GAL4, SEQ ID NO:32, to the N-terminal of human MVP, SEQ ID NO:1, and ANT, SEQ ID NO:72 to the C-terminal of human MVP, SEQ ID NO:1, to create GAL4-MVP-ANT, SEQ ID NO:96, encoded by the cDNA, SEQ ID NO:97. In another embodiment, the vault-like particle

comprises, consists essentially of, or consists of MVP modified by adding GAL4, SEQ ID NO:32, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, and ANT, SEQ ID NO:72 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create GAL4-MVP-ANT, SEQ ID NO:98, encoded by the cDNA, SEQ ID NO:99. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding GAL4, SEQ ID NO:32, to the N-terminal of human MVP, SEQ ID NO:1, and α CEA, SEQ ID NO:84 to the C-terminal of human MVP, SEQ ID NO:1, to create GAL4-MVP- α CEA, SEQ ID NO:100, encoded by the cDNA, SEQ ID NO:101. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding GAL4, SEQ ID NO:32, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, and α CEA, SEQ ID NO:84 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create GAL4-MVP- α CEA, SEQ ID NO:102, encoded by the cDNA, SEQ ID NO:103. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding GAL4, SEQ ID NO:32, to the N-terminal of human MVP, SEQ ID NO:1, and EGF, SEQ ID NO:90 to the C-terminal of human MVP, SEQ ID NO:1, to create GAL4-MVP-EGF, SEQ ID NO:104, encoded by the cDNA, SEQ ID NO:105. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding GAL4, SEQ ID NO:32, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, and EGF, SEQ ID NO:90 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create GAL4-MVP-EGF, SEQ ID NO:106, encoded by the cDNA, SEQ ID NO:107. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding GAL4, SEQ ID NO:32, to the N-terminal of human MVP, SEQ ID NO:1, and TAT, SEQ ID NO:78 to the C-terminal of human MVP, SEQ ID NO:1, to create GAL4-MVP-TAT, SEQ ID NO:108, encoded by the cDNA, SEQ ID NO:109. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding GAL4, SEQ ID NO:32, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:1, and TAT, SEQ ID NO:78 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create GAL4-MVP-TAT, SEQ ID NO:110, encoded by the cDNA, SEQ ID NO:111. In one embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding MS2, SEQ ID NO:38, to the N-terminal of human MVP, SEQ ID NO:1, and ANT, SEQ ID NO:72 to the C-terminal of human MVP, SEQ ID NO:1, to create MS2-MVP-ANT, SEQ ID NO:112,

encoded by the cDNA, SEQ ID NO:113. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding MS2, SEQ ID NO:38, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, and ANT, SEQ ID NO:72 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create MS2-MVP-ANT, SEQ ID NO:114, encoded by the cDNA, SEQ ID NO:115. In another embodiment, 5 the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding MS2, SEQ ID NO:38, to the N-terminal of human MVP, SEQ ID NO:1, and α CEA, SEQ ID NO:84 to the C-terminal of human MVP, SEQ ID NO:1, to create MS2-MVP- α CEA, SEQ ID NO:116, encoded by the cDNA, SEQ ID NO:117. In another embodiment, 10 the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding MS2, SEQ ID NO:38, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, and α CEA, SEQ ID NO:84 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create MS2-MVP- α CEA, SEQ ID NO:118, encoded by the cDNA, SEQ ID NO:119. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of 15 MVP modified by adding MS2, SEQ ID NO:38, to the N-terminal of human MVP, SEQ ID NO:1, and EGF, SEQ ID NO:90 to the C-terminal of human MVP, SEQ ID NO:1, to create MS2-MVP-EGF, SEQ ID NO:120, encoded by the cDNA, SEQ ID NO:121. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding MS2, SEQ ID NO:38, to the N-terminal of *Rattus norvegicus* MVP, SEQ 20 ID NO:10, and EGF, SEQ ID NO:90 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create MS2-MVP-EGF, SEQ ID NO:122, encoded by the cDNA, SEQ ID NO:123. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding MS2, SEQ ID NO:38, to the N-terminal of human MVP, SEQ ID NO:1, and TAT, SEQ ID NO:78 to the C-terminal of human MVP, SEQ ID 25 NO:1, to create MS2-MVP-TAT, SEQ ID NO:124, encoded by the cDNA, SEQ ID NO:125. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding MS2, SEQ ID NO:38, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:1, and TAT, SEQ ID NO:78 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create MS2-MVP-TAT, SEQ ID NO:126, encoded by the cDNA, 30 SEQ ID NO:127. In one embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding polylysine, SEQ ID NO:22, to the N-terminal of human MVP, SEQ ID NO:1, and ANT, SEQ ID NO:72 to the C-terminal of human MVP,

SEQ ID NO:1, to create polylysine-MVP-ANT, SEQ ID NO:128, encoded by the cDNA, SEQ ID NO:129. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding polylysine, SEQ ID NO:22, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, and ANT, SEQ ID NO:72 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create polylysine-MVP-ANT, SEQ ID NO:130, encoded by the cDNA, SEQ ID NO:131. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding polylysine, SEQ ID NO:22, to the N-terminal of human MVP, SEQ ID NO:1, and α CEA, SEQ ID NO:84 to the C-terminal of human MVP, SEQ ID NO:1, to create polylysine-MVP- α CEA, SEQ ID NO:132, encoded by the cDNA, SEQ ID NO:133. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding polylysine, SEQ ID NO:22, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, and α CEA, SEQ ID NO:84 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create polylysine-MVP- α CEA, SEQ ID NO:134, encoded by the cDNA, SEQ ID NO:135. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding polylysine, SEQ ID NO:22, to the N-terminal of human MVP, SEQ ID NO:1, and EGF, SEQ ID NO:90 to the C-terminal of human MVP, SEQ ID NO:1, to create polylysine-MVP-EGF, SEQ ID NO:136, encoded by the cDNA, SEQ ID NO:137. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding polylysine, SEQ ID NO:22, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, and EGF, SEQ ID NO:90 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create polylysine-MVP-EGF, SEQ ID NO:138, encoded by the cDNA, SEQ ID NO:139. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding polylysine, SEQ ID NO:22, to the N-terminal of human MVP, SEQ ID NO:1, and TAT, SEQ ID NO:78 to the C-terminal of human MVP, SEQ ID NO:1, to create polylysine-MVP-TAT, SEQ ID NO:140, encoded by the cDNA, SEQ ID NO:141. In another embodiment, the vault-like particle comprises, consists essentially of, or consists of MVP modified by adding polylysine, SEQ ID NO:22, to the N-terminal of *Rattus norvegicus* MVP, SEQ ID NO:1, and TAT, SEQ ID NO:78 to the C-terminal of *Rattus norvegicus* MVP, SEQ ID NO:10, to create polylysine-MVP-TAT, SEQ ID NO:142, encoded by the cDNA, SEQ ID NO:143.

According to another embodiment of the present invention, there is provided a vault-

like particle comprising MVP and VPARP or a portion of VPARP, where the MVP is modified by adding an amino acid sequence to the N-terminal or is modified by adding an amino acid sequence to the C-terminal, or is modified both by adding an amino acid sequence to the N-terminal and by adding an amino acid sequence to the C-terminal, and where the VPARP or portion of VPARP is modified by adding an amino acid sequence to the N-terminal or is modified by adding an amino acid sequence to the C-terminal, or is modified both by adding an amino acid sequence to the N-terminal and by adding an amino acid sequence to the C-terminal. The modifications can be any modification as disclosed in this disclosure, for the same purposes as disclosed in this disclosure.

In another embodiment of the present invention, there is provided a method of preventing damage by one or more than one substance to an organism, to a specific tissue, to specific cells, or to an environmental medium, by sequestering the one or more than one substance within a vault-like particle. The method comprises providing vault-like particles according to the present invention. The method further comprises administering the vault-like particles to the organism, tissue, cells or environmental medium, and allowing the vault-like particles to sequester the one or more than one substance within the vault-like particles. In one embodiment, the vault-like particles comprise, consist essentially of or consist of a modified MVP according to the present invention. In another embodiment, the vault-like particles comprise a modified VPARP or portion of VPARP according to the present invention. In another embodiment, the vault-like particles comprise both a modified MVP according to the present invention, and a modified VPARP or portion of VPARP according to the present invention. In a preferred embodiment, the vault-like particles comprise, consist essentially of or consist of MVP modified by adding a peptide to the N-terminal to create a one or more than one of heavy metal binding domains. In one embodiment, the one or more than one substance is a heavy metal selected from the group consisting of cadmium, copper, gold and mercury. In another embodiment, the one or more than one substance is a toxin selected from the group consisting of arsenate, dioxin, an organochlorine, a pentachlorophenol and a polychlorinated biphenyl. In a preferred embodiment, the providing step comprises expressing the vault-like particles in a eukaryotic organisms, such as for example an *Acanthamoeba* sp., yeast or *Dictostelium discoideum*, capable of proliferating in contaminated soil, and the administering step comprises introducing the organisms with the expressed vault-like particles into the contaminated soil. For example, vault-like particles

comprising an arsenate reductase enzyme within the vault-like particles can be expressed in the organisms and used to detoxify soil. For example, in one embodiment, modified MVP is provided comprising one or more than one arsenate-binding domain at the N-terminal.

Arsenate reductase enzyme is cloned with residues 1473-1724 of human VPARP, SEQ ID

5 NO:3 at either the C-terminal or the N-terminal. Both proteins are co-expressed in a primitive eukaryotic organisms, such as *acanthamoeba*, yeast or *Dictostelium discoideum*, capable of proliferating in contaminated soil. The organisms engineered to contain the two modified proteins are introduced into contaminated soil, where they are exposed to the environmental toxin, such as arsenate. The expressed vault-like particles, comprising 96 or
10 more copies of the arsenate-binding domain and the detoxification enzyme, arsenate reductase within the vault-like particles, then sequester and detoxify the environmental toxin, arsenate in the environmental medium.

In another embodiment of the present invention, there is provided a method of delivering one or more than one substance to an organism, to a specific tissue, to specific
15 cells, or to an environmental medium. The method comprises providing vault-like particles according to the present invention comprising the one or more than one substance. The method further comprises administering the vault-like particles comprising the one or more than one substance to the organism, tissue, cells or environmental medium. In one embodiment, the vault-like particles comprise, consist essentially of or consist of a modified
20 MVP according to the present invention, in addition to the one or more than one substance. In another embodiment, the vault-like particles comprise a modified VPARP or modified portion of VPARP according to the present invention. In another embodiment, the vault-like particles comprise both a modified MVP according to the present invention, and a modified VPARP or modified portion of VPARP according to the present invention. In a preferred
25 embodiment, the one or more than one substance is selected from the group consisting of an enzyme, a pharmaceutical agent, a plasmid, a polynucleotide, a polypeptide, a sensor and a combination of the preceding. In a particularly preferred embodiment, the substance is adenosine deaminase.

In another embodiment of the present invention, there is provided a method of
30 delivering one or more than one sensor to an organism, to a specific tissue, to specific cells, or to an environmental medium. The method comprises providing a vault-like particle comprising the one or more than one sensor and administering the vault-like particle to the

organism, specific tissue, specific cells, or environmental medium. In one embodiment, the vault-like particles comprise, consist essentially of or consist of a modified MVP according to the present invention, in addition to the one or more than one sensor. In another embodiment, the vault-like particles comprise a modified VPARP or modified portion of VPARP according to the present invention. In another embodiment, the vault-like particles comprise both a modified MVP according to the present invention, and a modified VPARP or modified portion of VPARP according to the present invention. The sensor can be any suitable sensor, as will be appreciated by one of ordinary skill in the art with reference to this disclosure, such as for example, a chemical sensor such as a cyclic-AMP binding protein, an ionic sensor such as a calcium or potassium sensor, a microorganism sensor such an antibody specific for *E. coli*, an optical sensor such as a quantum dot, and a pH sensor such as green fluorescence protein. In a preferred embodiment, the sensor is a fluorescent sensor.

In another embodiment, the present invention is a method of detecting a signal from a sensor within an organism, or a specific tissue or specific cells. The method comprises delivering one or more than one sensor to an organism, to a specific tissue, to specific cells, or to an environmental medium, according to a method of the present invention. Then, the presence of the sensor is detected. Detection is performed using standard techniques, such as for example, fluorometry or spectrophotometry. This method can be used, for example, to determine the pH within cells, where the sensor is a pH dependent fluorescent sensor, as will be appreciated by one of ordinary skill in the art with reference to this disclosure.

According to another embodiment of the present invention, there is provided a method of making vault-like particles according to the present invention. The method comprises creating polynucleotide sequences encoding one or more than one polypeptide selected from the group consisting of MVP, modified MVP, VPARP, a portion of VPARP, modified VPARP, a modified portion of VPARP, TEP1, a portion of TEP1, modified TEP1 and a modified portion of TEP1, using standard molecular biological procedures, such as polymerase chain reaction and specific oligonucleotides, as will be appreciated by one of ordinary skill in the art with reference to this disclosure. Preferably, the polynucleotide sequences are used to generate a bacmid DNA that is used to generate a baculovirus comprising the sequence. The baculovirus is then used to infect insect cells for protein production using an *in situ* assembly system, such as the baculovirus protein expression system, according to standard techniques, as will be appreciated by one of ordinary skill in

the art with reference to this disclosure. Advantageously, we have used the baculovirus protein expression system to produce milligram quantities of vault-like particles, and this system can be scaled up to allow production of gram quantities of vault-like particles according to the present invention.

5 In another embodiment of the present invention, there is provided a method of making vault-like particles having one or more than one substance, such as an enzyme, a pharmaceutical agent, a plasmid, a polynucleotide, a polypeptide, a sensor and a combination of the preceding, within the vault-like particles. The method comprises making the vault-like particles according to a method of the present invention. Next, the vault-like particles are
10 purified using, such as for example, standard procedures over sucrose gradients. Then, the vault-like particles are co-incubated with one or more than one substance, until the one or more than one substance equilibrates within the vault-like particles or until enough of the one or more than one substance is loaded in the vault-like particles for the intended purpose.

 Although the present invention has been discussed in considerable detail with
15 reference to certain preferred embodiments, other embodiments are possible. Therefore, the scope of the appended claims should not be limited to the description of preferred embodiments contained in this disclosure. All references cited herein are incorporated by reference to their entirety.

WHAT IS CLAIMED IS:

1. A method of using vaults as carrier molecules to deliver one or more than one substance to an organism, or to a specific tissue or to specific cells, or to an environmental medium, comprising:

- 5 a) providing vaults;
 b) incorporating the one or more than one substance into the vaults; and
 c) administering the vaults comprising the one or more than one substance to the organism, to the specific tissue, to the specific cells, or to the environmental medium.

10 2. The method of claim 1, where the vaults provided are purified from natural sources.

 3. The method of claim 1, where the vaults provided are generated using recombinant technology.

 4. The method of claim 1, where incorporation is accomplished by incubating the vaults with the one or more than one substance.

15 5. The method of claim 1, where the one or more than one substance is selected from the group consisting of an enzyme, a pharmaceutical agent, a plasmid, a polynucleotide, a polypeptide, a sensor and a combination of the preceding.

 6. A vault-like particle comprising MVP.

20 7. The vault-like particle of claim 6, further comprising VPARP or modified VPARP, or a portion of VPARP or a modified portion of VPARP.

 8. The vault-like particle of claim 6, further comprising TEP1 or modified TEP1, or a portion of TEP1 or a modified portion of TEP1.

 9. A vault-like particle comprising modified MVP.

25 10. The vault-like particle of claim 9, where the modified MVP comprises an amino acid sequence added to the N-terminal of the MVP which results in one or more than one substance-binding domain within the vault-like particle.

 11. The vault-like particle of claim 10, where the one or more than one substance-binding domain is between 1 and 95 substance-binding domains.

30 12. The vault-like particle of claim 10, where the one or more than one substance-binding domain is 96 substance-binding domains.

 13. The vault-like particle of claim 10, where the one or more than one substance-binding domain is greater than 96 substance-binding domains.

14. The vault-like particle of claim 10, where the one or more than one substance-binding domain within the vault-like particle is one or more than one heavy metal binding domain.

15. The vault-like particle of claim 14, where the one or more than one heavy metal binding domain binds a heavy metal selected from the group consisting of cadmium, copper, gold and mercury.

16. The vault-like particle of claim 14, where the peptide added to the N-terminal is a cysteine-rich peptide.

17. The vault-like particle of claim 10, where the one or more than one substance-binding domain within the vault-like particle is one or more than one polynucleotide-binding domain.

18. The vault-like particle of claim 17, where the one or more than one polynucleotide-binding domain is a non-specific polynucleotide-binding peptide.

19. The vault-like particle of claim 17, where the one or more than one polynucleotide-binding domain is a specific polynucleotide-binding peptide.

20. The vault-like particle of claim 9, where the modified MVP comprises an amino acid sequence added to the N-terminal of the MVP creates a sensor in the vault-like particle.

21. The vault-like particle of claim 20, where the sensor is selected from the group consisting of a chemical sensor, an ionic sensor, a microorganism sensor, an optical sensor and a pH sensor.

22. The vault-like particle of claim 20, where the sensor is a green fluorescent protein.

23. The vault-like particle of claim 9, where the modified MVP comprises an amino acid sequence added to the C-terminal of the MVP which results in one or more than one receptor-binding domain.

24. The vault-like particle of claim 23, where the one or more than one receptor-binding domain is between 1 and 95 receptor-binding domains.

25. The vault-like particle of claim 23, where the one or more than one receptor-binding domain is 96 receptor-binding domains.

26. The vault-like particle of claim 23, where the one or more than one receptor-binding domain is greater than 96 receptor-binding domains.

27. The vault-like particle of claim 23, where the one or more than one receptor-

binding domain is non-specific.

28. The vault-like particle of claim 23, where the one or more than one receptor-binding domain is specific.

5 29. The vault-like particle of claim 10, where the modified MVP further comprises an amino acid sequence added to the C-terminal of the MVP which results in one or more than one receptor-binding domain.

30. The vault-like particle of claim 29, where the one or more than one receptor-binding domain is between 1 and 95 receptor-binding domains.

10 31. The vault-like particle of claim 29, where the one or more than one receptor-binding domain is 96 receptor-binding domains.

32. The vault-like particle of claim 29, where the one or more than one receptor-binding domain, is greater than 96 receptor-binding domains.

33. The vault-like particle of claim 29, where the one or more than one receptor-binding domain is non-specific.

15 34. The vault-like particle of claim 29, where the one or more than one receptor-binding domain is specific.

35. The vault-like particle of claim 9, where the modified MVP comprises both an amino acid sequence added to the C-terminal of the MVP and an amino acid sequence added to the N-terminal of the MVP.

20 36. A vault-like particle comprising MVP or modified MVP, and further comprising VPARP or a portion of VPARP comprising at least about 150 consecutive residues of VPARP.

37. The vault-like particle of claim 36, where the portion of VPARP comprises residues from about residue 1562 to 1724 of human VPARP, SEQ ID NO:3.

25 38. The vault-like particle of claim 36, where the portion of VPARP comprises residues from about residue 1473 to 1724 of human VPARP, SEQ ID NO:3.

39. The vault-like particle of claim 36, where the VPARP or portion of VPARP is modified.

30 40. The vault-like particle of claim 39, where the modification comprises adding an amino acid sequence added to the C-terminal of the VPARP or portion of VPARP.

41. The vault-like particle of claim 39, where the modification comprises adding an amino acid sequence added to the N-terminal of the VPARP or portion of VPARP.

42. The vault-like particle of claim 39, where the modification comprises adding an amino acid sequence added to both the C-terminal and the N-terminal of the VPARP or portion of VPARP.

42. The vault-like particle of claim 36, where the modified MVP comprises an amino acid sequence added to the C-terminal of the MVP.

44. The vault-like particle of claim 36, where the modified MVP comprises an amino acid sequence added to the N-terminal of the MVP.

45. The vault-like particle of claim 36, where the modified MVP comprises both a peptide added to the C-terminal and a peptide added to the N-terminal.

46. A method of preventing damage by one or more than one substance to an organism, to a specific tissue, to specific cells, or to an environmental medium, by sequestering the one or more than one substance within a vault-like particle, comprising:

a) providing vault-like particles;

b) administering the vault-like particles to the organism, tissue, cells or environmental medium; and

c) allowing the vault-like particles to sequester the one or more than one substance within the vault-like particles.

47. The method of claim 46, where the one or more than one substance is a heavy metal selected from the group consisting of cadmium, copper, gold and mercury.

48. The method of claim 46, where the one or more than one substance is a toxin selected from the group consisting of arsenate, dioxin, an organochlorine, a pentachlorophenol and a polychlorinated biphenyl.

49. The method of claim 46, where providing the vault-like particles comprises expressing the vault-like particles in a eukaryotic organism.

50. A method of delivering one or more than one substance to an organism, to a specific tissue, to specific cells, or to an environmental medium, comprising:

a) providing vault-like particles comprising the one or more than one substance; and

b) administering the vault-like particles comprising the one or more than one substance to the organism, tissue, cells or environmental medium.

51. The method of claim 50, where the vault-like particles comprise, consist essentially of or consist of a modified MVP in addition to the one or more than one substance.

52. The method of claim 50, where the vault-like particles comprise a modified VPARP or modified portion of VPARP.

53. The method of claim 50, where the vault-like particles comprise both a modified MVP according to the present invention, and a modified VPARP or modified portion of VPARP.

54. The method of claim 50, where the one or more than one substance is selected from the group consisting of an enzyme, a pharmaceutical agent, a plasmid, a polynucleotide, a polypeptide, a sensor and a combination of the preceding.

55. The method of claim 50, where the one or more than one substance is adenosine deaminase.

56. A method of delivering one or more than one sensor to an organism, to a specific tissue, to specific cells, or to an environmental medium, comprising:

- a) providing a vault-like particle comprising the one or more than one sensor; and
- b) administering the vault-like particle to the organism, specific tissue, specific cells,

or environmental medium.

57. The method of claim 56, where the vault-like particles comprise, consist essentially of or consist of a modified MVP, in addition to the one or more than one sensor.

58. The method of claim 56, where the vault-like particles comprise a modified VPARP or modified portion of VPARP.

59. The method of claim 56, where the vault-like particles comprise both a modified MVP, and a modified VPARP or modified portion of VPARP.

60. The method of claim 56, where the sensor is selected from the group consisting of a chemical sensor, a fluorescent sensor, an ionic sensor, a microorganism sensor, an optical sensor, and a pH sensor.

61. A method of detecting a signal from a sensor within an organism, or a specific tissue or specific cells, comprising:

- a) delivering one or more than one sensor to an organism, to a specific tissue, to specific cells, or to an environmental medium according to claim 56; and
- b) detecting the presence of the sensor.

62. The method of claim 61, where detection is accomplished by fluorometry or by spectrophotometry.

63. A method of making vault-like particles comprising:

a) creating polynucleotide sequences encoding one or more than one polypeptide selected from the group consisting of MVP, modified MVP, VPARP, a portion of VPARP, modified VPARP, a modified portion of VPARP, TEP1, a portion of TEP1, modified TEP1 and a modified portion of TEP1;

- 5 b) using the polynucleotide sequences created to generate a bacmid DNA;
 c) using the bacmid DNA to generate a baculovirus comprising the sequence; and
 d) using the baculovirus to infect insect cells for protein production using an *in situ* assembly system.

64. A method of making vault-like particles comprising one or more than one
10 substance, the method comprising:

- a) making vault-like particles according to claim 63; and
 b) co-incubated the vault-like particles with the one or more than one substance.

65. The method of claim 64, where the one or more than one substance is selected
from the group consisting of enzyme, a pharmaceutical agent, a plasmid, a polynucleotide, a
15 polypeptide, a sensor and a combination of the preceding.

66. The method of claim 64, further comprising purifying the vault-like particles
after making the vault-like particles.

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Gly Ser Tyr Leu Thr Pro Thr Thr Arg Ala His Ser Pro Ala Ser
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Leu Ser Phe Ala Ser Tyr Arg Gln Val Ala Ser Phe Gly Ser Ala
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Ala Pro Pro Arg Gln Phe Asp Ala Ser Gln Phe Ser Gln Gly Pro

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Phe Pro Glu Leu Asp Ser Pro	Gln Leu His Phe Ser	Leu Pro Thr
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Lys Leu His Gln His Val Ser Thr His Ser Asp Ile Leu Ser Leu Lys
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Asn Gln Cys Leu Ala Thr Leu Pro Asp Leu Lys Thr Met Glu Lys Pro
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His Gly Tyr Val Ser Ala His Pro Asp Ile Leu Ser Leu Glu Asn Gln
65 70 75 80

Cys Leu Ala Thr Leu Ser Asp Leu Lys Thr Met Glu Lys Pro His Gly
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His Val Ser Ala His Pro Asp Ile Leu Ser Leu Glu Asn Arg Cys Leu
100 105 110

Ala Thr Leu Pro Ser Leu Lys Ser Thr Val Ser Ala Ser Pro Leu Phe
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Gln Ser Leu Gln Ile Ser His Met Thr Gln Ala Asp Leu Tyr Arg Val
130 135 140

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His Phe Ser Lys Gly Leu Asp Leu Ser Thr Cys Pro Ile Ala Leu Lys
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Ser Ile Ser Ala Thr Glu Thr Ala Gln Glu Ala Thr Leu Gly Arg Trp
180 185 190

Phe Asp Ser Glu Glu Lys Lys Gly Ala Glu Thr Gln Met Pro Ser Tyr
195 200 205

Ser Leu Ser Leu Gly Glu Glu Glu Glu Val Glu Asp Leu Ala Val Lys
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Leu Thr Ser Gly Asp Ser Glu Ser His Pro Glu Pro Thr Asp His Val
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Leu Gln Glu Lys Lys Met Ala Leu Leu Ser Leu Leu Cys Ser Thr Leu
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Val Ser Glu Val Asn Met Asn Asn Thr Ser Asp Pro Thr Leu Ala Ala
 260 265 270

Ile Phe Glu Ile Cys Arg Glu Leu Ala Leu Leu Glu Pro Glu Phe Ile
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Leu Lys Ala Ser Leu Tyr Ala Arg Gln Gln Leu Asn Val Arg Asn Val
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Ala Asn Asn Ile Leu Ala Ile Ala Ala Phe Leu Pro Ala Cys Arg Pro
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His Leu Arg Arg Tyr Phe Cys Ala Ile Val Gln Leu Pro Ser Asp Trp
 325 330 335

Ile Gln Val Ala Glu Leu Tyr Gln Ser Leu Ala Glu Gly Asp Lys Asn
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Lys Leu Val Pro Leu Pro Ala Cys Leu Arg Thr Ala Met Thr Asp Lys
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Phe Ala Gln Phe Asp Glu Tyr Gln Leu Ala Lys Tyr Asn Pro Arg Lys
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His Arg Ala Lys Arg His Pro Arg Arg Pro Pro Arg Ser Pro Gly Met
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Glu Pro Pro Phe Ser His Arg Cys Phe Pro Arg Tyr Ile Gly Phe Leu
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Arg Glu Glu Gln Arg Lys Phe Glu Lys Ala Gly Asp Thr Val Ser Glu
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Lys Lys Asn Pro Pro Arg Phe Thr Leu Lys Lys Leu Val Gln Arg Leu
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His Ile His Lys Pro Ala Gln His Val Gln Ala Leu Leu Gly Tyr Arg
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Tyr Pro Ser Asn Leu Gln Leu Phe Ser Arg Ser Arg Leu Pro Gly Pro
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Trp Asp Ser Ser Arg Ala Gly Lys Arg Met Lys Leu Ser Arg Pro Glu

20/429

Val Val Leu Cys Gly Gly Asp Thr Leu Lys Thr Ala Val Leu Lys Ala
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Glu Phe Asp Glu Asn Asp Gly Trp Ser Leu Asn Thr Phe Gly Lys Tyr
755 760 765

Leu Leu Ser Leu Ala Gly Gln Arg Val Pro Val Asp Arg Val Ile Leu
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Leu Gly Gln Ser Met Asp Asp Gly Met Ile Asn Val Ala Lys Gln Leu
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Tyr Trp Gln Arg Val Asn Ser Lys Cys Leu Phe Val Gly Ile Leu Leu
805 810 815

Arg Arg Val Gln Tyr Leu Ser Thr Asp Leu Asn Pro Asn Asp Val Thr
820 825 830

Leu Ser Gly Cys Thr Asp Ala Ile Leu Lys Phe Ile Ala Glu His Gly
835 840 845

Ala Ser His Leu Leu Glu His Val Gly Gln Met Asp Lys Ile Phe Lys
850 855 860

Ile Pro Pro Pro Pro Gly Lys Thr Gly Val Gln Ser Leu Arg Pro Leu
865 870 875 880

Glu Glu Asp Thr Pro Ser Pro Leu Ala Pro Val Ser Gln Gln Gly Trp
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Arg Ser Ile Arg Leu Phe Ile Ser Ser Thr Phe Arg Asp Met His Gly
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Glu Arg Asp Leu Leu Leu Arg Ser Val Leu Pro Ala Leu Gln Ala Arg
915 920 925

Ala Ala Pro His Arg Ile Ser Leu His Gly Ile Asp Leu Arg Trp Gly
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Val Thr Glu Glu Glu Thr Arg Arg Asn Arg Gln Leu Glu Val Cys Leu
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Gly Glu Val Glu Asn Ala Gln Leu Phe Val Gly Ile Leu Gly Ser Arg
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Tyr Gly Tyr Ile Pro Pro Ser Tyr Asn Leu Pro Asp His Pro His Phe
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Pro His Gly Arg Leu Ser Leu Val Thr Gly Gln Ser Gly Gln Gly
 1160 1165 1170

Lys Thr Ala Phe Leu Ala Ser Leu Val Ser Ala Leu Gln Ala Pro

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Cys Thr Tyr Leu Arg Gly Gln Leu Lys Glu Pro Gly Ala Leu Pro		
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Ser Thr Tyr Arg Ser Leu Val Trp Glu Leu Gln Gln Arg Leu Leu		
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Pro Lys Ser Ala Glu Ser Leu His Pro Gly Gln Thr Gln Val Leu		
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Leu Arg Trp Leu Asn Lys Pro Arg Thr Met Lys Asn Gln Gln Ser
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Phe Ser Thr Asn Gly Gln Arg Ala Ala Val Gly Thr Ala Asn Gly
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Thr Val Tyr Leu Leu Asp Leu Arg Thr Trp Gln Glu Glu Lys Ser
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Ser Trp Ala Gly Ser Ile Ser Phe Phe Gln Val Asp Gly Leu Lys
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Val Thr Lys Asp Leu Gly Ala Pro Gly Ala Ser Ile Arg Thr Leu

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1910	1915	1920
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1925	1930	1935
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2015	2020	2025
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Arg Pro His Lys Ala Glu Asp	Phe Pro Cys Gly Thr	Glu Leu Arg
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Asp	Val	Arg	Thr	Pro	Lys	Thr	Pro	Val	Leu	Ile	His	Ser	Phe	Pro
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Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 675	680	685
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys 690	695	700
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly 705	710	715
		720

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 725 730 735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
 755 760 765

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 770 775 780

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 785 790 795 800

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 820 825 830

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
 835 840 845

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
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gtggccaacc ctgtgtccccg ggacaccag agttctgtgt tatttgacat cacaggacaa 240

gtccgactcc ggcacgctga ccaggagatc cgactagccc aggaccctt cccctgtat 300

ccaggggagg tgctggaaaa ggacatcacc ccaactgcagg tggttctgcc caacacagca 360

ctgcatctta aggcgttgct ggactttgag gataagaatg gagacaaggc catggcagga 420

gacgagtggc tatttgaggg acctggcacc tacatccac agaaggaagt ggaagtcgtg 480

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cgtgtccgc acaatgcagc ggtgcaggtc tatgactaca gagccaagag agcccggtgtg	1440
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cagtcagtgg agcccggtga ccagaggacc cgggatgccc ttcagcgcag cgttcagctg	1980
gccatcgaaa ttaccaccaa ctcccaggag gcagcagcca agcacgaggc tcagagactg	2040
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aagtga 2586

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<213> Rattus norvegicus

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<400> 12

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```

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Leu Lys Asn Arg Cys Leu Thr Met Leu Ser Asp Ile Gln Pro Leu Glu
20           25           30

```

```

Lys Ile His Gly Gln Arg Ser Val Asn Pro Asp Ile Leu Ser Leu Glu
35           40           45

```

```

Asn Arg Cys Leu Thr Leu Leu Pro Asp Leu Gln Pro Met Glu Lys Ile
50           55           60

```

```

His Gly Gln Arg Ser Val His Pro Asp Ile Leu Ser Ser Glu Asn Arg
65           70           75           80

```

```

Cys Leu Thr Leu Leu Pro Asp Leu Gln Ser Leu Glu Lys Leu Cys Gly
85           90           95

```

```

His Met Ser Ser His Pro Asp Val Leu Ser Leu Glu Asn Arg Cys Leu
100          105          110

```

```

Ala Thr Leu Pro Thr Val Lys Arg Thr Val Ser Ser Gly Pro Leu Leu
115          120          125

```

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Gln Cys Leu His Arg Ser His Thr Ala Gln Ala Asp Leu Arg Asp Pro
130          135          140

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Asn Phe Arg Asn Cys Leu Phe Pro Glu Pro Pro Thr Ile Glu Ala Pro
 145 150 155 160

Cys Phe Leu Lys Glu Leu Asp Leu Pro Thr Gly Pro Arg Ala Leu Lys
 165 170 175

Ser Met Ser Ala Thr Ala Arg Val Gln Glu Val Ala Leu Gly Gln Arg
 180 185 190

Cys Val Ser Glu Gly Lys Glu Leu Gln Glu Glu Lys Glu Ser Ala Glu
 195 200 205

Val Pro Met Pro Leu Tyr Ser Leu Ser Leu Gly Gly Glu Glu Glu Glu
 210 215 220

Val Val Gly Ala Pro Val Leu Lys Leu Thr Ser Gly Asp Ser Asp Ser
 225 230 235 240

His Pro Glu Thr Thr Asp Gln Ile Leu Gln Glu Lys Lys Met Ala Leu
 245 250 255

Leu Thr Leu Leu Cys Ser Ala Met Ala Ser Ser Val Asn Val Lys Asp
 260 265 270

Ala Ser Asp Pro Thr Arg Ala Ser Ile His Glu Val Cys Ser Ala Leu
 275 280 285

Ala Pro Leu Glu Pro Glu Phe Ile Leu Lys Ala Ser Leu Tyr Ala Arg
 290 295 300

Gln Gln Leu Asn Leu Arg Asp Ile Ala Asn Ile Val Leu Ala Val Ala
 305 310 315 320

Ala Leu Leu Pro Ala Cys Arg Pro His Val Arg Arg Tyr Tyr Ser Ala
 325 330 335

Ile Val His Leu Pro Ser Asp Trp Ile Gln Val Ala Glu Phe Tyr Gln
 340 345 350

Ser Leu Ala Glu Gly Asp Glu Lys Lys Leu Val Pro Leu Pro Ala Cys
 355 360 365

Leu Arg Ala Ala Met Thr Asp Lys Phe Ala Gln Phe Asp Glu Tyr Gln
 370 375 380

Leu Ala Lys Tyr Asn Pro Arg Lys His Arg Ser Lys Thr Arg Ser Arg
 385 390 395 400
 Gln Pro Pro Arg Pro Gln Arg Thr Lys Pro Pro Phe Ser Glu Ser Gly
 405 410 415
 Lys Cys Phe Pro Lys Ser Val Trp Pro Leu Lys Asn Glu Gln Ile Ser
 420 425 430
 Phe Glu Ala Ala Tyr Asn Ala Val Ser Glu Lys Lys Arg Leu Pro Arg
 435 440 445
 Phe Thr Leu Lys Lys Leu Val Glu Gln Leu His Ile His Glu Pro Ala
 450 455 460
 Gln His Val Gln Ala Leu Leu Gly Tyr Arg Tyr Pro Ser Thr Leu Glu
 465 470 475 480
 Leu Phe Ser Arg Ser His Leu Pro Gly Pro Trp Asp Ser Ser Arg Ala
 485 490 495
 Gly Gln Arg Met Lys Leu Gln Arg Pro Glu Thr Trp Glu Arg Glu Leu
 500 505 510
 Ser Leu Arg Gly Asn Arg Ala Ser Val Trp Glu Glu Leu Ile Asp Asn
 515 520 525
 Gly Lys Leu Pro Phe Met Ala Met Leu Arg Asn Leu Cys Asn Leu Leu
 530 535 540
 Arg Thr Gly Ile Ser Ala His His His Glu Leu Val Leu Gln Arg Leu
 545 550 555 560
 Gln His Glu Lys Ser Val Ile His Ser Arg Gln Phe Pro Phe Arg Phe
 565 570 575
 Leu Asn Ala His Asp Ser Leu Asp Arg Leu Glu Ala Gln Leu Arg Ser
 580 585 590
 Lys Ala Ser Pro Phe Pro Ser Asn Thr Thr Leu Met Lys Arg Ile Met
 595 600 605
 Ile Arg Asn Ser Lys Lys Ile Lys Arg Pro Ala Asn Pro Arg Tyr Leu

610	615	620
Cys Thr Leu Thr Gln Arg Gln Leu Arg Ala Ala Met Ala Ile Pro Val		
625	630	635 640
Met Tyr Glu His Leu Lys Arg Glu Lys Leu Arg Leu His Lys Ala Arg		
	645	650 655
Gln Trp Thr Cys Asp Leu Glu Leu Leu Glu Arg Tyr Arg Gln Ala Leu		
	660	665 670
Glu Thr Ala Val Asn Ile Ser Val Lys His Asn Leu Pro Pro Leu Pro		
	675	680 685
Gly Arg Thr Leu Leu Val Tyr Leu Thr Asp Ala Asn Ala Asn Arg Leu		
	690	695 700
Cys Pro Lys Ser His Leu Gln Gly Pro Pro Leu Asn Tyr Val Leu Leu		
	705	710 715 720
Leu Ile Gly Met Met Met Ala Arg Ala Glu Gln Thr Thr Val Trp Leu		
	725	730 735
Cys Gly Thr Gly Thr Val Lys Thr Pro Val Leu Thr Ala Asp Glu Gly		
	740	745 750
Ile Leu Lys Thr Ala Ile Lys Leu Gln Ala Gln Val Gln Glu Leu Glu		
	755	760 765
Glu Asn Asp Glu Trp Pro Leu Glu Thr Phe Glu Lys Tyr Leu Leu Ser		
	770	775 780
Leu Ala Val Arg Arg Thr Pro Ile Asp Arg Val Ile Leu Phe Gly Gln		
	785	790 795 800
Arg Met Asp Thr Glu Leu Leu Asn Val Ala Lys Gln Ile Ile Trp Gln		
	805	810 815
His Val Asn Ser Lys Cys Leu Phe Val Ser Val Leu Leu Arg Lys Met		
	820	825 830
Gln Tyr Met Ser Pro Asn Leu Asn Pro Asn Asp Val Thr Leu Ser Gly		
	835	840 845

Cys Thr Asp Gly Ile Leu Lys Phe Ile Ala Glu His Gly Ala Ser Arg
 850 855 860

Leu Leu Glu His Val Gly Gln Leu Asp Lys Ile Phe Lys Ile Pro Pro
 865 870 875 880

Pro Pro Gly Lys Thr Lys Val Ser Pro Leu Arg Pro Leu Glu Glu Asn
 885 890 895

Asn Pro Gly Pro Phe Val Pro Ile Ser Gln His Gly Trp Arg Asn Ile
 900 905 910

Arg Leu Phe Ile Ser Ser Thr Phe Arg Asp Met His Gly Glu Arg Asp
 915 920 925

Leu Leu Met Arg Ser Val Leu Pro Ala Leu Gln Ala Arg Ala Phe Pro
 930 935 940

His Arg Ile Ser Leu His Ala Ile Asp Leu Arg Trp Gly Ile Thr Glu
 945 950 955 960

Glu Glu Thr Arg Arg Asn Arg Gln Leu Glu Val Cys Leu Gly Glu Val
 965 970 975

Glu Asn Ser Gln Leu Phe Val Gly Ile Leu Gly Ser Arg Tyr Gly Tyr
 980 985 990

Thr Pro Pro Ser Tyr Asp Leu Pro Asp His Pro His Phe His Trp Thr
 995 1000 1005

Gln Arg Tyr Pro Ser Gly Arg Ser Val Thr Glu Met Glu Val Met
 1010 1015 1020

Gln Phe Leu Asn Arg Gly Gln Arg Ser Glu Pro Ser Asp Gln Ala
 1025 1030 1035

Leu Ile Tyr Phe Arg Asp Pro Gly Phe Leu Ser Ser Val Pro Asp
 1040 1045 1050

Val Trp Lys Pro Asp Phe Ile Ser Glu Ser Glu Glu Ala Ala His
 1055 1060 1065

Arg Val Ser Glu Leu Lys Arg Phe Leu Gln Glu Gln Lys Glu Val
 1070 1075 1080

Thr Cys	Arg Arg Tyr Ser Cys	Glu Trp Gly Gly Val	Ala Ala Gly
1085	1090	1095	
Arg Pro	Tyr Thr Gly Gly Leu	Glu Glu Phe Gly Gln	Leu Val Leu
1100	1105	1110	
Gln Asp	Val Trp Ser Val Ile	Gln Lys Arg Tyr Leu	Gln Pro Gly
1115	1120	1125	
Ala Gln	Leu Glu Gln Pro Gly	Ser Ile Ser Glu Glu	Asp Leu Ile
1130	1135	1140	
Gln Ala	Ser Phe Gln Gln Leu	Lys Ser Pro Pro Ser	Pro Ala Arg
1145	1150	1155	
Pro Arg	Leu Leu Gln Asp Thr	Val Gln Gln Leu Met	Leu Pro His
1160	1165	1170	
Gly Arg	Leu Ser Leu Val Ile	Gly Gln Ala Gly Gln	Gly Lys Thr
1175	1180	1185	
Ala Phe	Leu Ala Ser Leu Val	Ser Ala Leu Lys Val	Pro Asp Gln
1190	1195	1200	
Pro Asn	Val Ala Pro Phe Val	Phe Phe His Phe Ser	Ala Ala Arg
1205	1210	1215	
Pro Asp	Gln Cys Leu Ala Phe	Asn Leu Leu Arg Arg	Leu Cys Thr
1220	1225	1230	
His Leu	His Gln Lys Leu Gly	Glu Pro Ser Ala Leu	Pro Ser Thr
1235	1240	1245	
Tyr Arg	Gly Leu Val Trp Glu	Leu Gln Gln Lys Leu	Leu Leu Lys
1250	1255	1260	
Ser Ala	Gln Trp Leu Gln Pro	Gly Gln Thr Leu Val	Leu Ile Ile
1265	1270	1275	
Asp Gly	Ala Asp Lys Leu Val	Asp His Asn Gly Gln	Leu Ile Ser
1280	1285	1290	
Asp Trp	Ile Pro Lys Ser Leu	Pro Arg Arg Val His	Leu Val Leu

1295		1300		1305
Ser Val	Ser Ser Asp Ser	Gly Leu Gly Glu Thr	Leu Gln Gln Ser	
1310		1315		1320
Gln Ser	Ala Tyr Val Val	Ala Leu Gly Ser Leu	Val Pro Ser Ser	
1325		1330		1335
Arg Ala	Gln Leu Val Arg	Glu Glu Leu Ala Leu	Tyr Gly Lys Arg	
1340		1345		1350
Leu Glu	Glu Ser Pro Phe	Asn Asn Gln Met Arg	Leu Leu Leu Ala	
1355		1360		1365
Lys Gln	Gly Ser Ser Leu	Pro Leu Tyr Leu His	Leu Val Thr Asp	
1370		1375		1380
Tyr Leu	Arg Leu Phe Thr	Leu Tyr Glu Gln Val	Ser Glu Arg Leu	
1385		1390		1395
Arg Thr	Leu Pro Ala Thr	Leu Pro Leu Leu Leu	Gln His Ile Leu	
1400		1405		1410
Ser Thr	Leu Glu Gln Glu	His Gly His Asn Val	Leu Pro Gln Ala	
1415		1420		1425
Leu Thr	Ala Leu Glu Val	Thr His Ser Gly Leu	Thr Val Asp Gln	
1430		1435		1440
Leu His	Ala Val Leu Ser	Thr Trp Leu Thr Leu	Pro Lys Glu Thr	
1445		1450		1455
Lys Ser	Trp Glu Glu Ala	Val Ala Ala Ser His	Ser Gly Asn Leu	
1460		1465		1470
Tyr Pro	Leu Ala Pro Phe	Ala Tyr Leu Val Gln	Ser Leu Arg Ser	
1475		1480		1485
Leu Leu	Gly Glu Gly Pro	Val Glu Arg Pro Gly	Ala Arg Leu Cys	
1490		1495		1500
Leu Ser	Asp Gly Pro Leu	Arg Thr Ala Val Lys	Arg Arg Tyr Gly	
1505		1510		1515

Lys	Arg	Leu	Gly	Leu	Glu	Lys	Thr	Ala	His	Val	Leu	Ile	Ala	Ala
1520						1525					1530			
His	Leu	Trp	Lys	Met	Cys	Asp	Pro	Asp	Ala	Ser	Gly	Thr	Phe	Arg
1535						1540					1545			
Ser	Cys	Pro	Pro	Glu	Ala	Leu	Lys	Asp	Leu	Pro	Tyr	His	Leu	Leu
1550						1555					1560			
Gln	Ser	Gly	Asn	His	Gly	Leu	Leu	Ala	Lys	Phe	Leu	Thr	Asn	Leu
1565						1570					1575			
His	Val	Val	Ala	Ala	Tyr	Leu	Glu	Val	Gly	Leu	Val	Pro	Asp	Leu
1580						1585					1590			
Leu	Glu	Ala	Tyr	Glu	Leu	Tyr	Ala	Ser	Ser	Lys	Pro	Glu	Val	Asn
1595						1600					1605			
Gln	Lys	Leu	Pro	Glu	Ala	Asp	Val	Ala	Val	Phe	His	Asn	Phe	Leu
1610						1615					1620			
Lys	Gln	Gln	Ala	Ser	Leu	Leu	Thr	Gln	Tyr	Pro	Leu	Leu	Leu	Leu
1625						1630					1635			
Gln	Gln	Ala	Ala	Ser	Gln	Pro	Glu	Glu	Ser	Pro	Val	Cys	Cys	Gln
1640						1645					1650			
Ala	Pro	Leu	Leu	Thr	Gln	Arg	Trp	His	Asn	Gln	Cys	Ile	Leu	Lys
1655						1660					1665			
Trp	Ile	Asn	Lys	Pro	Gln	Thr	Leu	Lys	Gly	Gln	Gln	Ser	Leu	Ser
1670						1675					1680			
Leu	Pro	Ile	Ser	Ser	Ser	Pro	Thr	Ala	Val	Ala	Phe	Ser	Pro	Asn
1685						1690					1695			
Gly	Gln	Arg	Ala	Ala	Val	Gly	Thr	Ala	Gly	Gly	Thr	Ile	Tyr	Leu
1700						1705					1710			
Leu	Asn	Leu	Arg	Thr	Trp	Gln	Glu	Glu	Lys	Ala	Leu	Val	Ser	Gly
1715						1720					1725			
Cys	Asp	Gly	Ile	Ser	Ser	Phe	Ala	Phe	Leu	Ser	Asp	Thr	Ala	Leu
1730						1735					1740			

Phe	Leu	Thr	Thr	Phe	Asp	Gly	Leu	Leu	Glu	Leu	Trp	Asp	Leu	Gln
1745						1750					1755			
His	Gly	Cys	Trp	Val	Phe	Gln	Thr	Lys	Ala	His	Gln	Tyr	Gln	Ile
1760						1765					1770			
Thr	Gly	Cys	Cys	Leu	Ser	Pro	Asp	Arg	Arg	Leu	Leu	Ala	Thr	Val
1775						1780					1785			
Cys	Leu	Gly	Gly	Tyr	Val	Lys	Leu	Trp	Asp	Thr	Val	Gln	Gly	Gln
1790						1795					1800			
Leu	Ala	Phe	Gln	Tyr	Thr	His	Pro	Lys	Ser	Leu	Asn	Cys	Ile	Thr
1805						1810					1815			
Phe	His	Pro	Glu	Gly	Gln	Val	Val	Ala	Thr	Gly	Asn	Trp	Ser	Gly
1820						1825					1830			
Ile	Val	Thr	Phe	Phe	Gln	Ala	Asp	Gly	Leu	Lys	Val	Thr	Lys	Glu
1835						1840					1845			
Leu	Gly	Gly	Pro	Gly	Pro	Ser	Val	Arg	Thr	Leu	Ala	Phe	Ser	Ala
1850						1855					1860			
Pro	Gly	Lys	Val	Val	Ala	Leu	Gly	Arg	Ile	Asp	Gly	Thr	Val	Glu
1865						1870					1875			
Leu	Trp	Ala	Trp	Gln	Glu	Gly	Thr	Arg	Leu	Ala	Ala	Phe	Pro	Ala
1880						1885					1890			
Gln	Cys	Gly	Gly	Val	Ser	Thr	Val	Leu	Phe	Leu	His	Ala	Gly	Gly
1895						1900					1905			
Arg	Phe	Leu	Thr	Ala	Gly	Glu	Asp	Gly	Lys	Ala	Gln	Leu	Trp	Ser
1910						1915					1920			
Gly	Phe	Leu	Gly	Arg	Pro	Arg	Gly	Cys	Leu	Gly	Ser	Leu	Tyr	Leu
1925						1930					1935			
Ser	Pro	Ala	Leu	Ser	Val	Ala	Leu	Asn	Pro	Asp	Gly	Asp	Gln	Val
1940						1945					1950			
Ala	Val	Gly	Tyr	Arg	Gly	Asp	Gly	Ile	Lys	Ile	Tyr	Arg	Ile	Ser

1955	1960	1965
Ser Gly Pro Gln Glu Ala 1970	Gln Cys Gln Glu Leu 1975	Asn Val Ala Val 1980
Ser Ala Leu Val Trp Leu 1985	Ser Pro Ser Val Leu 1990	Val Ser Gly Ala 1995
Glu Asp Gly Ser Leu His 2000	Gly Trp Met Leu Arg 2005	Arg Asn Ser Leu 2010
Gln Ser Leu Trp Leu Ser 2015	Ser Val Cys Gln Lys 2020	Pro Val Leu Gly 2025
Leu Ala Ala Ser Gln Glu 2030	Phe Leu Ala Ser Ala 2035	Ser Glu Asp Phe 2040
Thr Val Arg Leu Trp Pro 2045	Arg Gln Leu Leu Thr 2050	Gln Pro His Ala 2055
Val Glu Glu Leu Pro Cys 2060	Ala Ala Glu Leu Arg 2065	Gly His Glu Gly 2070
Pro Val Cys Cys Cys Ser 2075	Phe Ser Pro Asp Gly 2080	Arg Ile Leu Ala 2085
Thr Ala Gly Arg Asp Arg 2090	Asn Leu Leu Cys Trp 2095	Asp Val Lys Val 2100
Ala Gln Ala Pro Leu Leu 2105	Ile His Thr Phe Ser 2110	Ser Cys His Arg 2115
Asp Trp Ile Thr Gly Cys 2120	Thr Trp Thr Lys Asp 2125	Asn Ile Leu Ile 2130
Ser Cys Ser Ser Asp Gly 2135	Ser Val Gly Leu Trp 2140	Asn Pro Glu Ala 2145
Gly Gln Gln Leu Gly Gln 2150	Phe Pro Gly His Gln 2155	Ser Ala Val Ser 2160
Ala Val Val Ala Val Glu 2165	Glu His Ile Val Ser 2170	Val Ser Arg Asp 2175

Gly Thr Leu Lys Val Trp Asp Arg Gln Gly Val Glu Leu Thr Ser
 2180 2185 2190

Ile Pro Ala His Ser Gly Pro Ile Ser Gln Cys Ala Ala Ala Leu
 2195 2200 2205

Glu Pro Arg Pro Ala Gly Gln Pro Gly Ser Glu Leu Met Val Val
 2210 2215 2220

Thr Val Gly Leu Asp Gly Ala Thr Lys Leu Trp His Pro Leu Leu
 2225 2230 2235

Val Cys Gln Ile His Thr Leu Gln Gly His Ser Gly Pro Val Thr
 2240 2245 2250

Ala Ala Ala Ala Ser Glu Ala Ser Gly Leu Leu Leu Thr Ser Asp
 2255 2260 2265

Asn Ser Ser Val Arg Leu Trp Gln Ile Pro Lys Glu Ala Asp Asp
 2270 2275 2280

Thr Cys Lys Pro Arg Ser Ser Ala Val Ile Thr Ala Val Ala Trp
 2285 2290 2295

Ala Pro Asp Gly Ser Leu Val Val Ser Gly Asn Glu Ala Gly Glu
 2300 2305 2310

Leu Thr Leu Trp Gln Lys Ala Gln Ala Val Ala Thr Ala Arg Ala
 2315 2320 2325

Pro Gly Arg Val Ser Asp Leu Ile Trp Cys Ser Ala Asn Ala Phe
 2330 2335 2340

Phe Val Leu Ser Ala Asn Glu Asn Val Ser Glu Trp Gln Val Glu
 2345 2350 2355

Leu Arg Lys Gly Ser Thr Cys Thr Asn Phe Arg Leu Tyr Leu Lys
 2360 2365 2370

Arg Val Leu Gln Glu Asp Leu Gly Val Leu Thr Gly Met Ala Leu
 2375 2380 2385

Ala Pro Asp Gly Gln Ser Leu Ile Leu Met Lys Glu Asp Val Glu
 2390 2395 2400

Leu	Leu	Gln	Met	Lys	Pro	Gly	Ser	Thr	Pro	Ser	Ser	Ile	Cys	Arg
2405						2410					2415			
Arg	Tyr	Ala	Val	His	Ser	Ser	Ile	Leu	Cys	Thr	Ser	Lys	Asp	Tyr
2420						2425					2430			
Gly	Leu	Phe	Tyr	Leu	Gln	Gln	Gly	Asn	Ser	Gly	Ser	Leu	Ser	Ile
2435						2440					2445			
Leu	Glu	Gln	Glu	Glu	Ser	Gly	Lys	Phe	Glu	Lys	Thr	Leu	Asp	Phe
2450						2455					2460			
Asn	Leu	Asn	Leu	Asn	Asn	Pro	Asn	Gly	Ser	Pro	Val	Ser	Ile	Thr
2465						2470					2475			
Gln	Ala	Glu	Pro	Glu	Ser	Gly	Ser	Ser	Leu	Leu	Cys	Ala	Thr	Ser
2480						2485					2490			
Asp	Gly	Met	Leu	Trp	Asn	Leu	Ser	Glu	Cys	Thr	Pro	Glu	Gly	Glu
2495						2500					2505			
Trp	Val	Val	Asp	Asn	Ile	Trp	Gln	Lys	Lys	Ser	Arg	Asn	Pro	Lys
2510						2515					2520			
Ser	Arg	Thr	Pro	Gly	Thr	Asp	Ser	Ser	Pro	Gly	Leu	Phe	Cys	Met
2525						2530					2535			
Asp	Ser	Trp	Val	Glu	Pro	Thr	His	Leu	Lys	Ala	Arg	Gln	Cys	Lys
2540						2545					2550			
Lys	Ile	His	Leu	Gly	Ser	Val	Thr	Ala	Leu	His	Val	Leu	Pro	Gly
2555						2560					2565			
Leu	Leu	Val	Thr	Ala	Ser	Glu	Asp	Arg	Asp	Val	Lys	Leu	Trp	Glu
2570						2575					2580			
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Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro Val Ser Arg Asp
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Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln Val Arg Leu Arg
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His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro Phe Pro Leu Tyr
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Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln Val Val Leu
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Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe Glu Asp Lys
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Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu Phe Glu Gly Pro
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Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val Glu Ile Ile Gln
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Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu Ala His Val
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Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro Ile Thr Thr Leu
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Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val Gly Pro Asp Gly
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Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile Gln Asp Val Tyr
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Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala Lys Val Glu

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Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp Pro Leu Ala Asp
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Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp His Phe Glu
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Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln Gln Leu Ala
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 caggccttgg ccattgaaac ggaggctgag ctccagaggg tccagaaggt ccgagagctg 2340
 gaactggtct atgcccgggc ccagctggag ctggagggtga gcaaggctca gcagctggct 2400
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 gaccttgctg tggctgggccc tgagatgcag gtaaaactgc tccagtccct gggcctgaaa 2520
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2718

<210> 18
 <211> 873
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 18

Met Ala Gly Cys Gly Cys Pro Cys Gly Cys Gly Ala Met Ala Thr Glu
 1 5 10 15

Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile His Val Leu Asp
 20 25 30

Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys Thr Tyr Ile
 35 40 45

Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val Arg Met Val Thr
 50 55 60

Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro Val Ser Arg Asp
 65 70 75 80

Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln Val Arg Leu Arg
 85 90 95

His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro Phe Pro Leu Tyr
 100 105 110

Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln Val Val Leu
 115 120 125

Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe Glu Asp Lys
 130 135 140

Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu Phe Glu Gly Pro
 145 150 155 160

Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val Glu Ile Ile Gln
 165 170 175

Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu Arg Ala Arg Lys

180 185 190
 Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr Gly Glu Glu Trp
 195 200 205
 Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val Phe Glu Glu Val
 210 215 220
 Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr Ala Leu His
 225 230 235 240
 Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly Val Leu His Arg
 245 250 255
 Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu Ala His Val
 260 265 270
 Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro Ile Thr Thr Leu
 275 280 285
 Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met Gly Pro Asp Gly
 290 295 300
 Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu Lys Ser Phe
 305 310 315 320
 Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile Gln Asp Val Tyr
 325 330 335
 Val Leu Ser Glu Gln Gln Gly Leu Leu Lys Ala Leu Gln Pro Leu
 340 345 350
 Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln Ala Gly Asp Cys
 355 360 365
 Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala Lys Val Glu
 370 375 380
 Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln Asn Glu Gly Ile
 385 390 395 400
 Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val Ile Gly Ser
 405 410 415

Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys Glu Leu Pro
 420 425 430

Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp Pro Leu Ala Asp
 435 440 445

Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro Ser Ala Pro Arg
 450 455 460

Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn Ala Ala Val
 465 470 475 480

Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val Val Phe Gly Pro
 485 490 495

Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr Val Leu Ser Leu
 500 505 510

Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala Leu Cys Leu
 515 520 525

Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile Glu Thr Ala
 530 535 540

Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp His Phe Glu
 545 550 555 560

Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys Leu Phe Ser Val
 565 570 575

Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser Arg Val Arg
 580 585 590

Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys Asn Ser Ala
 595 600 605

Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met Ser Glu Asp Thr
 610 615 620

Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp Gln Ala Val Phe
 625 630 635 640

Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln Ser Val Glu
 645 650 655

Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser Val Gln Leu
660 665 670

Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala Lys His Glu
675 680 685

Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu Arg Gln Lys
690 695 700

Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu Leu Leu Glu
705 710 715 720

Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly Asn Ala Lys Ala
725 730 735

Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly Glu Gly Ser
740 745 750

Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile Glu Thr Glu
755 760 765

Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met Glu Leu Ile Tyr
770 775 780

Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln Gln Leu Ala
785 790 795 800

Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu Ala Leu Gly Pro
805 810 815

Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met Gln Val Lys
820 825 830

Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr Asp Gly Ser
835 840 845

Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu Leu Gly Leu Gly
850 855 860

Ser Asp Gly Gln Pro Pro Ala Gln Lys
865 870

<210> 19

<211> 2622
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 19
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 gaggttggtgac caaagacctc catccggcag gacaatgaga gggactgtgt tgcgccagtt 180
 cgcatggtga ccgtccccc acgccactac tgcatagtgg ccaaccctgt gtcccgggac 240
 acccagagtt ctgtgttatt tgacatcaca ggacaagtcc gactccggca cgctgaccag 300
 gagatccgac tagcccagga ccccttcccc ctgtatccag gggaggtgct ggaaaaggac 360
 atcacccac tgcagggtgt tctgcccac acagcactgc atcttaaggc gttgctggac 420
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 ggcacctaca tcccacagaa ggaagtggaa gtcgtggaga tcattcaggc cacagtcac 540
 aaacagaacc aagcactgcg gctaagggcc cgaaaggagt gctttgaccg ggagggcaag 600
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 tcagctccaa ggaacaagac ccgagtggtc agctaccgtg tcccgacaa tgcagcgggtg 1440
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ctggatcctg aggagcagtt cacagtattg tccctttctg ccgggcgacc caagcgtcct 1560
 catgcccgcc gtgcactctg cctactgctg ggacctgatt tctttactga tgtcatcacc 1620
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 ctgaagaacc ggaatgaccc tgcagaggca gccaaagcttt tctccgtgcc tgacttcgtg 1740
 ggtgacgcct gcaaggccat tgcacccga gtccgggggg ctgtagcctc tgtcaccttt 1800
 gatgacttcc ataaaaactc agcccggatc attcgaatgg ctgttttttg ctttgagatg 1860
 tctgaagaca caggtcctga tggcacactc ctgcccagg ctcgagacca ggcagtcttt 1920
 ccccaaaacg ggctggtagt cagcagtgtg gatgtgcagt cagtggagcc cgtggaccag 1980
 aggacccggg atgcccttca ggcagcgtt cagctggcca tcgaaattac caccaactcc 2040
 caggaggcag cagccaagca cgaggctcag agactggaac aggaagcccg tggtcggctt 2100
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 caggcgctag ccattgagac ggaggctgag ttggagcgag taaagaaagt acgagagatg 2340
 gaactgatct atgcccgggc ccagttggag ctggagggtga gcaaggcgca gcagcttgcc 2400
 aatgtggagg caaagaagtt caaggagatg acagaggcac tgggccccgg caccatcagg 2460
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 tccactctca tcaccgatgg ctgctctccc atcaacctct tcagcacagc cttcggggtg 2580
 ctggggctgg ggtctgatgg tcagccgcca gcacagaagt ga 2622

<210> 20

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> completely synthesized

<400> 20

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
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Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Pro	Trp
			20					25					30	

<210> 21

<211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> completely synthesized

<400> 21
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 atggctagca tgactggtgg acagcaacc 89

<210> 22
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> completely synthesized

<400> 22
 Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
 1 5 10 15

Pro

<210> 23
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> completely synthesized

<400> 23
 atgaagaaga agaagaagaa gaagaagaag aagaagaaga agaagaagcc c 51

<210> 24
 <211> 923
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

<400> 24
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Pro Met Ala

20 25 30
 Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile His Val
 35 40 45
 Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys Thr
 50 55 60
 Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met Arg Met
 65 70 75 80
 Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro Val Ser
 85 90 95
 Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln Val Arg
 100 105 110
 Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro Phe Pro
 115 120 125
 Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln Val
 130 135 140
 Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe Glu
 145 150 155 160
 Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu Phe Glu
 165 170 175
 Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val Glu Ile
 180 185 190
 Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu Arg Ala
 195 200 205
 Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr Gly Glu
 210 215 220
 Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val Phe Glu
 225 230 235 240
 Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr Ala
 245 250 255

Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly Val Ser
 260 265 270

Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu Ala
 275 280 285

His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro Ile Thr
 290 295 300

Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val Gly Pro
 305 310 315 320

Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu Lys
 325 330 335

Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile Gln Asp
 340 345 350

Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala Leu Gln
 355 360 365

Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln Ala Gly
 370 375 380

Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala Lys
 385 390 395 400

Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu Asn Glu
 405 410 415

Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val Ile
 420 425 430

Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys Glu
 435 440 445

Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp Pro Leu
 450 455 460

Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro Leu Ala
 465 470 475 480

Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn Ala
 485 490 495

Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val Val Phe
500 505 510

Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr Val Leu
515 520 525

Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala Leu
530 535 540

Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile Glu
545 550 555 560

Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp His
565 570 575

Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys Leu Phe
580 585 590

Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser Arg
595 600 605

Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys Asn
610 615 620

Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr Ser Glu
625 630 635 640

Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp Gln Ala
645 650 655

Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln Ser
660 665 670

Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser Val
675 680 685

Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala Lys
690 695 700

His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu Arg
705 710 715 720

Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu Leu

725

730

735

Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly Thr Ala
 740 745 750

Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly Glu
 755 760 765

Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile Glu
 770 775 780

Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu Glu Leu
 785 790 795 800

Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln Gln
 805 810 815

Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu Ala Ile
 820 825 830

Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met Gln
 835 840 845

Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr Asp
 850 855 860

Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu Leu Gly
 865 870 875 880

Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser Gly Pro
 885 890 895

Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro Gln Ala
 900 905 910

Pro Gly Asp Asn His Val Val Pro Val Leu Arg
 915 920

<210> 25

<211> 2772

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 25
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 ccccatacc actatatcca tgtgctggac cagaacagca acgtgtcccg tgtggaggtc 180
 gggccaaaga cctacatccg gcaggacaat gagaggggtac tgtttgcccc catgcgcatg 240
 gtgaccgtcc ccccacgtca ctactgcaca gtggccaacc ctgtgtctcg ggatgccag 300
 ggcttggtgc tgtttgatgt cacagggcaa gttcggcttc gccacgctga cctcgagatc 360
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 cccctgcagg tggttctgcc caacactgcc ctccatctaa aggcgctgct tgattttgag 480
 gataaagatg gagacaaggt ggtggcagga gatgagtggc ttttcgaggg acctggcacg 540
 tacatcccc ggaaggaagt ggaggtcgtg gagatcattc aggccaccat catcaggcag 600
 aaccaggctc tgcggctcag ggcccgaag gagtgtctgg accgggacgg caaggagagg 660
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atggggcccg agggctcagc cctgggcaga aggggtggcca gtgggcccag ccctggggag 2700
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gtactgcgct aa 2772

<210> 26

<211> 910

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 26

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
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Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr
20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg

515	520	525
Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile		
530	535	540
Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr		
545	550	555
Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala		
565	570	575
Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile		
580	585	590
Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe		
595	600	605
His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu		
610	615	620
Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg		
625	630	635
Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp		
645	650	655
Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln		
660	665	670
Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala		
675	680	685
Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg		
690	695	700
Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg		
705	710	715
Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr		
725	730	735
Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile		
740	745	750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu
 770 775 780

Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
 785 790 795 800

Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr
 805 810 815

Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
 835 840 845

Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala
 865 870 875 880

Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala
 885 890 895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg
 900 905 910

<210> 27

<211> 2733

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 27

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 aacgtgtccc gtgtggaggt cgggccaaag acctacatcc ggcaggacaa tgagagggta 180
 ctgtttgccc ccatgcgcat ggtgaccgtc cccccacgtc actactgcac agtggccaac 240
 cctgtgtctc gggatgccca gggcttggtg ctgtttgatg tcacagggca agttcggctt 300

cgccacgctg acctcgagat cgggctggcc caggaccctt tccccctgta cccaggggag	360
gtgctggaaa aggacatcac acccctgcag gtggttctgc ccaacactgc cctccatcta	420
aaggcgctgc ttgattttga ggataaagat ggagacaagg tggtaggcagg agatgagtgg	480
cttttcgagg gacctggcac gtacatcccc cggaaggaag tggaggtcgt ggagatcatt	540
caggccacca tcatcaggca gaaccaggct ctgcggctca gggcccgcaa ggagtgcagg	600
gaccgggacg gcaaggagag ggtgacaggg gaagaatggc tggtcaccac agtaggggag	660
tacctcccag cgggtgtttga ggaggttctg gatattgtgg acgccgtcat ccttacggaa	720
aagacagccc tgcacctccg ggctcggcgg aacttcgggg acttcagggg agtgccccgc	780
cgcactgggg aggagtggct ggtaacagtg caggacacag agggccacgt gccagatgtc	840
cacgaggagg tgctgggggt tgtgcccato accaccctgg gccccacaa ctactgcgtg	900
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ggagacaacc acgtggtgcc tgtactgcgc taa 2733

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<210> 28
 <211> 892
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 28

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Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
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```

```

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Pro Trp Met
          20           25           30

```

```

Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile His
          35           40           45

```

```

Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys
          50           55           60

```

```

Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val Arg
65           70           75           80

```

```

Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro Val
          85           90           95

```

Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln Val
 100 105 110

Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro Phe
 115 120 125

Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln
 130 135 140

Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe
 145 150 155 160

Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu Phe
 165 170 175

Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val Glu
 180 185 190

Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu Arg
 195 200 205

Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr Gly
 210 215 220

Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val Phe
 225 230 235 240

Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr
 245 250 255

Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly Val
 260 265 270

Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu
 275 280 285

Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro Ile
 290 295 300

Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met Gly
 305 310 315 320

Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu
 325 330 335

Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile Gln
 340 345 350

Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala Leu
 355 360 365

Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln Ala
 370 375 380

Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala
 385 390 395 400

Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln Asn
 405 410 415

Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val
 420 425 430

Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys
 435 440 445

Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp Pro
 450 455 460

Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro Ser
 465 470 475 480

Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn
 485 490 495

Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val Val
 500 505 510

Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr Val
 515 520 525

Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala
 530 535 540

Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile
 545 550 555 560

Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp

84/429

Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln
805 810 815

Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu Ala
820 825 830

Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met
835 840 845

Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr
850 855 860

Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu Leu
865 870 875 880

Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
885 890

<210> 29

<211> 2679

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Rattus norvegicus

<400> 29

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atccccccat accactacat ccatgtgctg gaccagaaca gtaatgtgtc ccgtgtggag	180
gttggaacaa agacctacat ccggcaggac aatgagaggg tactgtttgc cccagttcgc	240
atggtgaccg tccccccacg ccactactgc atagtggcca accctgtgtc ccgggacacc	300
cagagttctg tgttatttga catcacagga caagtccgac tccggcacgc tgaccaggag	360
atccgactag cccaggaccc cttccccctg tatccagggg aggtgctgga aaaggacatc	420
acccactgc aggtgggttct gcccacaca gcaactgcac ttaaggcggt gctggacttt	480
gaggataaga atggagacaa ggtcatggca ggagacgagt ggctatttga gggacctggc	540
acctacatcc cacagaagga agtggaagtc gtggagatca ttcaggccac agtcatcaaa	600
cagaaccaag cactgcggct aagggcccga aaggagtgtt ttgaccggga gggcaagggg	660
cgcgtgacag gtgaggagtg gctggtccga tccgtggggg cttacctccc agctgtcttt	720
gaagaggtgc tggatctggt ggatgctgtg atccttacag aaaagactgc cctgcacctc	780

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caggggctgc tactgaaggc actgcagccc ctggaggagg gagagagcga ggagaaggtc	1140
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<210> 30
 <211> 878
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 30

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
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Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr
 20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val

165	170	175
Val Glu Ile Ile Gln Ala Thr Val	Ile Lys Gln Asn Gln Ala Leu Arg	
180	185	190
Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val		
195	200	205
Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala		
210	215	220
Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu		
225	230	235
Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg		
245	250	255
Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp		
260	265	270
Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val		
275	280	285
Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro		
290	295	300
Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys		
305	310	315
Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly		
325	330	335
Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys		
340	345	350
Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His		
355	360	365
Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro		
370	375	380
Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp		
385	390	395
		400

Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala
 675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg
 690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg
 705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr
 725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile
 740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu
 770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
 785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr
 805 810 815

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
 835 840 845

Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys

865

870

875

<210> 31
<211> 2637
<212> DNA
<213> Artificial Sequence

<220>
<223> synthesized and Rattus norvegicus

<400> 31
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<210> 32

<211> 96

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 32

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
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20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

<210> 33
 <211> 288
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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 tctcccaaaa ccaaaagggtc tccgctgact agggcacatc tgacagaagt ggaatcaagg 180
 ctagaaagac tggaacagct atttctactg atttttcctc gagaagacct tgacatgatt 240
 ttgaaaatgg attctttaca ggatataaaa gcattgttaa caggatta 288

<210> 34
 <211> 989
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> *Saccharomyces cerevisiae* and *Homo sapiens*

<400> 34

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
 1 5 10 15

Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 325 330 335

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 355 360 365

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 435 440 445

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 515 520 525

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro

530

535

540

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 545 550 555 560

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 565 570 575

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 625 630 635 640

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
 645 650 655

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
 690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
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Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
965 970 975

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg
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<210> 35

<211> 2970

<212> DNA

<213> Artificial Sequence

<220>

<223> *Saccharomyces cerevisiae* and *Homo sapiens*

<400> 35

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<210> 36

<211> 957

<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccharomyces cerevisiae* and *Rattus norvegicus*

<400> 36

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 245 250 255
 Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 260 265 270
 Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 275 280 285
 Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300
 Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320
 Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 325 330 335
 Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350
 Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 355 360 365
 Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 370 375 380
 Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400
 Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 405 410 415
 Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 420 425 430
 Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 435 440 445
 Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 450 455 460
 Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln

465 470 475 480
 Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495
 Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510
 Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 515 520 525
 Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 530 535 540
 Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 545 550 555 560
 Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 565 570 575
 Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 580 585 590
 Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605
 Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620
 Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 625 630 635 640
 Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys
 645 650 655
 Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 660 665 670
 Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685
 Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met
 690 695 700

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
805 810 815

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
835 840 845

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
850 855 860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
 945 950 955

<210> 37
 <211> 2874
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Saccharomyces cerevisiae* and *Rattus norvegicus*

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<210> 38
 <211> 130
 <212> PRT
 <213> Levivirus

<400> 38

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
 1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

Ile Tyr
 130

<210> 39

<211> 393

<212> DNA

<213> Levivirus

<400> 39

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 caggcttaca aagtaacctg tagcgttcgt cagagctctg cgcagaatcg caaatacacc 180
 atcaaagtcg aggtgcctaa agtggcaacc cagactgttg gtggtgtaga gtttctgtga 240
 gccgcatggc gttcgtactt aaatatggaa ctaaccattc caattttcgc tacgaattcc 300
 gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360
 tcagcaatcg cagcaaactc cggcatctac ccc 393

<210> 40
 <211> 1024
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens

<400> 40

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
 1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr
 130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
 145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
 165 170 175

Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val
 180 185 190

Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val
195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala
210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
245 250 255

Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp
260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val
275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala
290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu
305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu
325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp
355 360 365

Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val
370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly
385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu
405 410 415

Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu
 435 440 445

Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
 450 455 460

Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
 500 505 510

Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val
 530 535 540

Leu Trp Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys
 545 550 555 560

Gly Gln Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser
 565 570 575

Leu Gln Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg
 580 585 590

Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg
 595 600 605

Ala Arg Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu
 610 615 620

Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His
 625 630 635 640

Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp
 645 650 655

Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu

660	665	670
Ala Tyr Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu		
675	680	685
Thr Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys		
690	695	700
Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp		
705	710	715
Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly		
	725	730
		735
Phe Glu Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg		
	740	745
		750
Pro Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser		
	755	760
		765
Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala		
	770	775
		780
Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln		
785	790	795
		800
Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg		
	805	810
		815
Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys		
	820	825
		830
Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu		
	835	840
		845
Ser Thr Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala		
	850	855
		860
Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln		
865	870	875
		880
Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val		
	885	890
		895

Arg Glu Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val
 900 905 910

Ser Lys Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln
 915 920 925

Met Thr Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala
 930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
 945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala
 965 970 975

Phe Gly Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg
 980 985 990

Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala
 995 1000 1005

Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu
 1010 1015 1020

Arg

<210> 41
 <211> 3075
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens

<400> 41
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 atcaaagtcg aggtgcctaa agtggcaacc cagactgttg gtggtgtaga gcttcctgta 240
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 gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360
 tcagcaatcg cagcaaactc cggcatctac cccatggcaa ctgaagagtt catcatccgc 420

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cagggccttg tgctgtttga tgtcacaggg caagtccggc ttcgccacgc tgacctcgag	660
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acaccctgc aggtggttct gcccaacact gccctccatc taaaggcgct gcttgatttt	780
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cagaaccagg ctctgcggct cagggcccgc aaggagtgtt gggaccggga cggcaaggag	960
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gaaacggcgg atcatgccag gctgcaactg cagctggcct acaactggca ctttgagggtg	2040
aatgaccgga aggaccccca agagaocggc aagctctttt cagtgccaga ctttgtaggt	2100
gatgcctgca aagccatcgc atcccgggtg cggggggccg tggcctctgt cactttcgat	2160

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caaaacgggc tgggtggtcag cagtgtggac gtgcagtcag tggagcctgt ggatcagagg 2340
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gaagcggcgg ccaagcatga ggctcagaga ctggagcagg aagcccgcgg ccggcttgag 2460
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cctgtactgc gctaa 3075

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<210> 42
 <211> 992
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Levivirus and Rattus norvegicus

<400> 42

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Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
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Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
          20          25          30

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Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
          35          40          45

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Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
          50          55          60

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Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr
130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
165 170 175

Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val
180 185 190

Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile
195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala
210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
245 250 255

Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp
260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val
275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala
290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
 500 505 510

Leu Asp Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val

530	535	540
Leu Trp Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu		
545	550	555 560
Gly His Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro		
565	570	575
Leu Gln Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg		
580	585	590
Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg		
595	600	605
Ala Arg Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu		
610	615	620
Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His		
625	630	635 640
Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp		
645	650	655
Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu		
660	665	670
Ala Tyr Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu		
675	680	685
Ala Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys		
690	695	700
Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp		
705	710	715 720
Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly		
725	730	735
Phe Glu Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys		
740	745	750
Ala Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser		
755	760	765

Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala
 770 775 780

Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln
 785 790 795 800

Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg
 805 810 815

Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys
 820 825 830

Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu
 835 840 845

Ser Thr Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala
 850 855 860

Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln
 865 870 875 880

Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val
 885 890 895

Arg Glu Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val
 900 905 910

Ser Lys Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu
 915 920 925

Met Thr Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala
 930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
 945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala
 965 970 975

Phe Gly Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
 980 985 990

<210> 43

<211> 2979

<212> DNA

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus

<400> 43

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gaagaggtgc tggatctggt ggatgctgtg atccttacag aaaagactgc cctgcacctc	1080
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<210> 44

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> completely synthesized

<400> 44

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro
 225 230 235

<210> 45
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> completely synthesized

<400> 45
 atgagcaagg gcgaggaact gttcactggc gtgggtcccaa ttctcgtgga actggatggc 60
 gatgtgaatg ggcacaaatt ttctgtcagc ggagaggggtg aaggtgatgc cacatacggg 120
 aagctcaccc tgaaattcat ctgcaccact ggaaagctcc ctgtgccatg gccaacactg 180
 gtcactacct tcacctatgg cgtgcagtgc ttttccagat acccagacca tatgaagcag 240
 catgactttt tcaagagcgc catgcccagag ggctatgtgc aggagagAAC catctttttc 300
 aaagatgacg ggaactacaa gacccgcgct gaagtcaagt tcgaagggtga caccctgggtg 360
 aatagaatcg agctgaaggg cattgacttt aaggaggatg gaaacattct cggccacaag 420
 ctggaatata actataactc ccacaatgtg tacatcatgg ccgacaagca aaagaatggc 480
 atcaagggtca acttcaagat cagacacaaC attgaggatg gatccgtgca gctggccgac 540
 cattatcaac agaactctcc aatcggcgac ggccctgtgc tcttcccaga caaccattac 600
 ctgtccaccc agtctgccct gtctaaagat cccaacgaaa agagagacca catgggtcctg 660
 ctggagtttg tgaccgctgc tgggatcaca catggcatgg acgagctgta caagcccatg 720

<210> 46
 <211> 1132
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

<400> 46

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe

50	55	60
Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln 65 70 75 80		
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95		
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110		
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125		
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140		
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 145 150 155 160		
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175		
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro 180 185 190		
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser 195 200 205		
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val 210 215 220		
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Met 225 230 235 240		
Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile His 245 250 255		
Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys 260 265 270		
Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met Arg 275 280 285		

Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro Val
 290 295 300

Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln Val
 305 310 315 320

Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro Phe
 325 330 335

Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln
 340 345 350

Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe
 355 360 365

Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu Phe
 370 375 380

Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val Glu
 385 390 395 400

Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu Arg
 405 410 415

Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr Gly
 420 425 430

Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val Phe
 435 440 445

Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr
 450 455 460

Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly Val
 465 470 475 480

Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu
 485 490 495

Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro Ile
 500 505 510

Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val Gly
 515 520 525

Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu
 530 535 540

Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile Gln
 545 550 555 560

Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala Leu
 565 570 575

Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln Ala
 580 585 590

Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala
 595 600 605

Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu Asn
 610 615 620

Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val
 625 630 635 640

Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys
 645 650 655

Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp Pro
 660 665 670

Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro Leu
 675 680 685

Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn
 690 695 700

Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val Val
 705 710 715 720

Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr Val
 725 730 735

Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala
 740 745 750

Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile

755

760

765

Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp
 770 775 780

His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys Leu
 785 790 795 800

Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser
 805 810 815

Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys
 820 825 830

Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr Ser
 835 840 845

Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp Gln
 850 855 860

Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln
 865 870 875 880

Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser
 885 890 895

Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala
 900 905 910

Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu
 915 920 925

Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu
 930 935 940

Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly Thr
 945 950 955 960

Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly
 965 970 975

Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile
 980 985 990

Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu Glu
 995 1000 1005

Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 1010 1015 1020

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr
 1025 1030 1035

Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly
 1040 1045 1050

Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
 1055 1060 1065

Thr Leu Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr
 1070 1075 1080

Ala Phe Gly Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly
 1085 1090 1095

Arg Arg Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro
 1100 1105 1110

Gln Ser Ala Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val
 1115 1120 1125

Pro Val Leu Arg
 1130

<210> 47
 <211> 3399
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

<400> 47

Ala Thr Gly Ala Gly Cys Ala Ala Gly Gly Gly Cys Gly Ala Gly Gly
 1 5 10 15

Ala Ala Cys Thr Gly Thr Thr Cys Ala Cys Thr Gly Gly Cys Gly Thr
 20 25 30

Gly Gly Thr Cys Cys Cys Ala Ala Thr Thr Cys Thr Cys Gly Thr Gly
 35 40 45

Gly Ala Ala Cys Thr Gly Gly Ala Thr Gly Gly Cys Gly Ala Thr Gly
 50 55 60

Thr Gly Ala Ala Thr Gly Gly Gly Cys Ala Cys Ala Ala Ala Thr Thr
 65 70 75 80

Thr Thr Cys Thr Gly Thr Cys Ala Gly Cys Gly Gly Ala Gly Ala Gly
 85 90 95

Gly Gly Thr Gly Ala Ala Gly Gly Thr Gly Ala Thr Gly Cys Cys Ala
 100 105 110

Cys Ala Thr Ala Cys Gly Gly Ala Ala Ala Gly Cys Thr Cys Ala Cys
 115 120 125

Cys Cys Thr Gly Ala Ala Ala Thr Thr Cys Ala Thr Cys Thr Gly Cys
 130 135 140

Ala Cys Cys Ala Cys Thr Gly Gly Ala Ala Ala Gly Cys Thr Cys Cys
 145 150 155 160

Cys Thr Gly Thr Gly Cys Cys Ala Thr Gly Gly Cys Cys Ala Ala Cys
 165 170 175

Ala Cys Thr Gly Gly Thr Cys Ala Cys Thr Ala Cys Cys Thr Thr Cys
 180 185 190

Ala Cys Cys Thr Ala Thr Gly Gly Cys Gly Thr Gly Cys Ala Gly Thr
 195 200 205

Gly Cys Thr Thr Thr Thr Cys Cys Ala Gly Ala Thr Ala Cys Cys Cys
 210 215 220

Ala Gly Ala Cys Cys Ala Thr Ala Thr Gly Ala Ala Gly Cys Ala Gly
 225 230 235 240

Cys Ala Thr Gly Ala Cys Thr Thr Thr Thr Thr Cys Ala Ala Gly Ala
 245 250 255

Gly Cys Gly Cys Cys Ala Thr Gly Cys Cys Cys Gly Ala Gly Gly Gly
 260 265 270

Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Gly Ala Gly Ala
 275 280 285

Ala Cys Cys Ala Thr Cys Thr Thr Thr Thr Thr Cys Ala Ala Ala Gly
 290 295 300

Ala Thr Gly Ala Cys Gly Gly Gly Ala Ala Cys Thr Ala Cys Ala Ala
 305 310 315 320

Gly Ala Cys Cys Cys Gly Cys Gly Cys Thr Gly Ala Ala Gly Thr Cys
 325 330 335

Ala Ala Gly Thr Thr Cys Gly Ala Ala Gly Gly Thr Gly Ala Cys Ala
 340 345 350

Cys Cys Cys Thr Gly Gly Thr Gly Ala Ala Thr Ala Gly Ala Ala Thr
 355 360 365

Cys Gly Ala Gly Cys Thr Gly Ala Ala Gly Gly Gly Cys Ala Thr Thr
 370 375 380

Gly Ala Cys Thr Thr Thr Ala Ala Gly Gly Ala Gly Gly Ala Thr Gly
 385 390 395 400

Gly Ala Ala Ala Cys Ala Thr Thr Cys Thr Cys Gly Gly Cys Cys Ala
 405 410 415

Cys Ala Ala Gly Cys Thr Gly Gly Ala Ala Thr Ala Cys Ala Ala Cys
 420 425 430

Thr Ala Thr Ala Ala Cys Thr Cys Cys Cys Ala Cys Ala Ala Thr Gly
 435 440 445

Thr Gly Thr Ala Cys Ala Thr Cys Ala Thr Gly Gly Cys Cys Gly Ala
 450 455 460

Cys Ala Ala Gly Cys Ala Ala Ala Ala Gly Ala Ala Thr Gly Gly Cys
 465 470 475 480

Ala Thr Cys Ala Ala Gly Gly Thr Cys Ala Ala Cys Thr Thr Cys Ala
 485 490 495

Ala Gly Ala Thr Cys Ala Gly Ala Cys Ala Cys Ala Ala Cys Ala Thr

500	505	510
Thr Gly Ala Gly Gly Ala Thr Gly Gly Ala Thr Cys Cys Gly Thr Gly		
515	520	525
Cys Ala Gly Cys Thr Gly Gly Cys Cys Gly Ala Cys Cys Ala Thr Thr		
530	535	540
Ala Thr Cys Ala Ala Cys Ala Gly Ala Ala Cys Ala Cys Thr Cys Cys		
545	550	555
Ala Ala Thr Cys Gly Gly Cys Gly Ala Cys Gly Gly Cys Cys Cys Thr		
565	570	575
Gly Thr Gly Cys Thr Cys Cys Thr Cys Cys Cys Ala Gly Ala Cys Ala		
580	585	590
Ala Cys Cys Ala Thr Thr Ala Cys Cys Thr Gly Thr Cys Cys Ala Cys		
595	600	605
Cys Cys Ala Gly Thr Cys Thr Gly Cys Cys Cys Thr Gly Thr Cys Thr		
610	615	620
Ala Ala Ala Gly Ala Thr Cys Cys Cys Ala Ala Cys Gly Ala Ala Ala		
625	630	635
Ala Gly Ala Gly Ala Gly Ala Cys Cys Ala Cys Ala Thr Gly Gly Thr		
645	650	655
Cys Cys Thr Gly Cys Thr Gly Gly Ala Gly Thr Thr Thr Gly Thr Gly		
660	665	670
Ala Cys Cys Gly Cys Thr Gly Cys Thr Gly Gly Gly Ala Thr Cys Ala		
675	680	685
Cys Ala Cys Ala Thr Gly Gly Cys Ala Thr Gly Gly Ala Cys Gly Ala		
690	695	700
Gly Cys Thr Gly Thr Ala Cys Ala Ala Gly Cys Cys Cys Ala Thr Gly		
705	710	715
Gly Cys Ala Ala Cys Thr Gly Ala Ala Gly Ala Gly Thr Thr Cys Ala		
725	730	735

Thr Cys Ala Thr Cys Cys Gly Cys Ala Thr Cys Cys Cys Cys Cys Cys
 740 745 750

Ala Thr Ala Cys Cys Ala Cys Thr Ala Thr Ala Thr Cys Cys Ala Thr
 755 760 765

Gly Thr Gly Cys Thr Gly Gly Ala Cys Cys Ala Gly Ala Ala Cys Ala
 770 775 780

Gly Cys Ala Ala Cys Gly Thr Gly Thr Cys Cys Cys Gly Thr Gly Thr
 785 790 795 800

Gly Gly Ala Gly Gly Thr Cys Gly Gly Gly Cys Cys Ala Ala Ala Gly
 805 810 815

Ala Cys Cys Thr Ala Cys Ala Thr Cys Cys Gly Gly Cys Ala Gly Gly
 820 825 830

Ala Cys Ala Ala Thr Gly Ala Gly Ala Gly Gly Gly Thr Ala Cys Thr
 835 840 845

Gly Thr Thr Thr Gly Cys Cys Cys Cys Cys Ala Thr Gly Cys Gly Cys
 850 855 860

Ala Thr Gly Gly Thr Gly Ala Cys Cys Gly Thr Cys Cys Cys Cys Cys
 865 870 875 880

Cys Ala Cys Gly Thr Cys Ala Cys Thr Ala Cys Thr Gly Cys Ala Cys
 885 890 895

Ala Gly Thr Gly Gly Cys Cys Ala Ala Cys Cys Cys Thr Gly Thr Gly
 900 905 910

Thr Cys Thr Cys Gly Gly Gly Ala Thr Gly Cys Cys Cys Ala Gly Gly
 915 920 925

Gly Cys Thr Thr Gly Gly Thr Gly Cys Thr Gly Thr Thr Gly Ala
 930 935 940

Thr Gly Thr Cys Ala Cys Ala Gly Gly Gly Cys Ala Ala Gly Thr Thr
 945 950 955 960

Cys Gly Gly Cys Thr Thr Cys Gly Cys Cys Ala Cys Gly Cys Thr Gly
 965 970 975

Ala Cys Cys Thr Cys Gly Ala Gly Ala Thr Cys Cys Gly Gly Cys Thr
 980 985 990

Gly Gly Cys Cys Cys Ala Gly Gly Ala Cys Cys Cys Cys Thr Thr Cys
 995 1000 1005

Cys Cys Cys Cys Thr Gly Thr Ala Cys Cys Cys Ala Gly Gly Gly
 1010 1015 1020

Gly Ala Gly Gly Thr Gly Cys Thr Gly Gly Ala Ala Ala Ala Gly
 1025 1030 1035

Gly Ala Cys Ala Thr Cys Ala Cys Ala Cys Cys Cys Cys Thr Gly
 1040 1045 1050

Cys Ala Gly Gly Thr Gly Gly Thr Thr Cys Thr Gly Cys Cys Cys
 1055 1060 1065

Ala Ala Cys Ala Cys Thr Gly Cys Cys Cys Thr Cys Cys Ala Thr
 1070 1075 1080

Cys Thr Ala Ala Ala Gly Gly Cys Gly Cys Thr Gly Cys Thr Thr
 1085 1090 1095

Gly Ala Thr Thr Thr Thr Gly Ala Gly Gly Ala Thr Ala Ala Ala
 1100 1105 1110

Gly Ala Thr Gly Gly Ala Gly Ala Cys Ala Ala Gly Gly Thr Gly
 1115 1120 1125

Gly Thr Gly Gly Cys Ala Gly Gly Ala Gly Ala Thr Gly Ala Gly
 1130 1135 1140

Thr Gly Gly Cys Thr Thr Thr Thr Cys Gly Ala Gly Gly Gly Ala
 1145 1150 1155

Cys Cys Thr Gly Gly Cys Ala Cys Gly Thr Ala Cys Ala Thr Cys
 1160 1165 1170

Cys Cys Cys Cys Gly Gly Ala Ala Gly Gly Ala Ala Gly Thr Gly
 1175 1180 1185

Gly Ala Gly Gly Thr Cys Gly Thr Gly Gly Ala Gly Ala Thr Cys

1190		1195		1200
Ala Thr Thr Cys Ala Gly Gly Cys Cys Ala Cys Cys Ala Thr Cys				
1205		1210		1215
Ala Thr Cys Ala Gly Gly Cys Ala Gly Ala Ala Cys Cys Ala Gly				
1220		1225		1230
Gly Cys Thr Cys Thr Gly Cys Gly Gly Cys Thr Cys Ala Gly Gly				
1235		1240		1245
Gly Cys Cys Cys Gly Cys Ala Ala Gly Gly Ala Gly Thr Gly Cys				
1250		1255		1260
Thr Gly Gly Gly Ala Cys Cys Gly Gly Gly Ala Cys Gly Gly Cys				
1265		1270		1275
Ala Ala Gly Gly Ala Gly Ala Gly Gly Gly Thr Gly Ala Cys Ala				
1280		1285		1290
Gly Gly Gly Gly Ala Ala Gly Ala Ala Thr Gly Gly Cys Thr Gly				
1295		1300		1305
Gly Thr Cys Ala Cys Cys Ala Cys Ala Gly Thr Ala Gly Gly Gly				
1310		1315		1320
Gly Cys Gly Thr Ala Cys Cys Thr Cys Cys Cys Ala Gly Cys Gly				
1325		1330		1335
Gly Thr Gly Thr Thr Thr Gly Ala Gly Gly Ala Gly Gly Thr Thr				
1340		1345		1350
Cys Thr Gly Gly Ala Thr Thr Thr Gly Gly Thr Gly Gly Ala Cys				
1355		1360		1365
Gly Cys Cys Gly Thr Cys Ala Thr Cys Cys Thr Thr Ala Cys Gly				
1370		1375		1380
Gly Ala Ala Ala Ala Gly Ala Cys Ala Gly Cys Cys Cys Thr Gly				
1385		1390		1395
Cys Ala Cys Cys Thr Cys Cys Gly Gly Gly Cys Thr Cys Gly Gly				
1400		1405		1410

Cys Gly Gly Ala Ala Cys Thr Thr Cys Cys Gly Gly Gly Ala Cys
 1415 1420 1425

Thr Thr Cys Ala Gly Gly Gly Ala Gly Thr Gly Thr Cys Cys
 1430 1435 1440

Cys Gly Cys Cys Gly Cys Ala Cys Thr Gly Gly Gly Gly Ala Gly
 1445 1450 1455

Gly Ala Gly Thr Gly Gly Cys Thr Gly Gly Thr Ala Ala Cys Ala
 1460 1465 1470

Gly Thr Gly Cys Ala Gly Gly Ala Cys Ala Cys Ala Gly Ala Gly
 1475 1480 1485

Gly Cys Cys Cys Ala Cys Gly Thr Gly Cys Cys Ala Gly Ala Thr
 1490 1495 1500

Gly Thr Cys Cys Ala Cys Gly Ala Gly Gly Ala Gly Gly Thr Gly
 1505 1510 1515

Cys Thr Gly Gly Gly Gly Gly Thr Thr Gly Thr Gly Cys Cys Cys
 1520 1525 1530

Ala Thr Cys Ala Cys Cys Ala Cys Cys Cys Thr Gly Gly Gly Cys
 1535 1540 1545

Cys Cys Cys Cys Ala Cys Ala Ala Cys Thr Ala Cys Thr Gly Cys
 1550 1555 1560

Gly Thr Gly Ala Thr Thr Cys Thr Cys Gly Ala Cys Cys Cys Thr
 1565 1570 1575

Gly Thr Cys Gly Gly Ala Cys Cys Gly Gly Ala Thr Gly Gly Cys
 1580 1585 1590

Ala Ala Gly Ala Ala Thr Cys Ala Gly Cys Thr Gly Gly Gly Gly
 1595 1600 1605

Cys Ala Gly Ala Ala Gly Cys Gly Cys Gly Thr Gly Gly Thr Cys
 1610 1615 1620

Ala Ala Gly Gly Gly Ala Gly Ala Gly Ala Ala Gly Thr Cys Thr
 1625 1630 1635

Thr Thr Thr Thr Thr Cys Cys Thr Cys Cys Ala Gly Cys Cys Ala
1640 1645 1650

Gly Gly Ala Gly Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala
1655 1660 1665

Cys Ala Ala Gly Gly Cys Ala Thr Cys Cys Ala Gly Gly Ala Thr
1670 1675 1680

Gly Thr Gly Thr Ala Thr Gly Thr Gly Cys Thr Gly Thr Cys Gly
1685 1690 1695

Gly Ala Gly Cys Ala Gly Cys Ala Gly Gly Gly Gly Cys Thr Gly
1700 1705 1710

Cys Thr Gly Cys Thr Gly Ala Gly Gly Gly Cys Cys Cys Thr Gly
1715 1720 1725

Cys Ala Gly Cys Cys Cys Cys Thr Gly Gly Ala Gly Gly Ala Gly
1730 1735 1740

Gly Gly Gly Gly Ala Gly Gly Ala Thr Gly Ala Gly Gly Ala Gly
1745 1750 1755

Ala Ala Gly Gly Thr Cys Thr Cys Ala Cys Ala Cys Cys Ala Gly
1760 1765 1770

Gly Cys Thr Gly Gly Gly Gly Ala Cys Cys Ala Cys Thr Gly Gly
1775 1780 1785

Cys Thr Cys Ala Thr Cys Cys Gly Cys Gly Gly Ala Cys Cys Cys
1790 1795 1800

Cys Thr Gly Gly Ala Gly Thr Ala Thr Gly Thr Gly Cys Cys Ala
1805 1810 1815

Thr Cys Thr Gly Cys Cys Ala Ala Ala Gly Thr Gly Gly Ala Gly
1820 1825 1830

Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly Cys Gly Cys
1835 1840 1845

Cys Ala Gly Gly Cys Cys Ala Thr Cys Cys Cys Thr Cys Thr Ala

1850	1855	1860
Gly Ala Cys Gly Ala Gly Ala Ala Cys Gly Ala Gly Gly Gly Cys		
1865	1870	1875
Ala Thr Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Thr		
1880	1885	1890
Gly Thr Cys Ala Ala Gly Ala Cys Cys Gly Gly Ala Ala Ala Gly		
1895	1900	1905
Gly Thr Gly Cys Gly Cys Gly Cys Thr Gly Thr Gly Ala Thr Thr		
1910	1915	1920
Gly Gly Ala Ala Gly Cys Ala Cys Cys Thr Ala Cys Ala Thr Gly		
1925	1930	1935
Cys Thr Gly Ala Cys Cys Cys Ala Gly Gly Ala Cys Gly Ala Ala		
1940	1945	1950
Gly Thr Cys Cys Thr Gly Thr Gly Gly Gly Ala Gly Ala Ala Ala		
1955	1960	1965
Gly Ala Gly Cys Thr Gly Cys Cys Thr Cys Cys Cys Gly Gly Gly		
1970	1975	1980
Gly Thr Gly Gly Ala Gly Gly Ala Gly Cys Thr Gly Cys Thr Gly		
1985	1990	1995
Ala Ala Cys Ala Ala Gly Gly Gly Gly Cys Ala Gly Gly Ala Cys		
2000	2005	2010
Cys Cys Thr Cys Thr Gly Gly Cys Ala Gly Ala Cys Ala Gly Gly		
2015	2020	2025
Gly Gly Thr Gly Ala Gly Ala Ala Gly Gly Ala Cys Ala Cys Ala		
2030	2035	2040
Gly Cys Thr Ala Ala Gly Ala Gly Cys Cys Thr Cys Cys Ala Gly		
2045	2050	2055
Cys Cys Cys Thr Thr Gly Gly Cys Gly Cys Cys Cys Cys Gly Gly		
2060	2065	2070

Ala	Ala	Cys	Ala	Ala	Gly	Ala	Cys	Cys	Cys	Gly	Thr	Gly	Thr	Gly
2075						2080					2085			
Gly	Thr	Cys	Ala	Gly	Cys	Thr	Ala	Cys	Cys	Gly	Cys	Gly	Thr	Gly
2090						2095					2100			
Cys	Cys	Cys	Cys	Ala	Cys	Ala	Ala	Cys	Gly	Cys	Thr	Gly	Cys	Gly
2105						2110					2115			
Gly	Thr	Gly	Cys	Ala	Gly	Gly	Thr	Gly	Thr	Ala	Cys	Gly	Ala	Cys
2120						2125					2130			
Thr	Ala	Cys	Cys	Gly	Ala	Gly	Ala	Gly	Ala	Ala	Gly	Cys	Gly	Ala
2135						2140					2145			
Gly	Cys	Cys	Cys	Gly	Cys	Gly	Thr	Gly	Gly	Thr	Cys	Thr	Thr	Cys
2150						2155					2160			
Gly	Gly	Gly	Cys	Cys	Thr	Gly	Ala	Gly	Cys	Thr	Gly	Gly	Thr	Gly
2165						2170					2175			
Thr	Cys	Gly	Cys	Thr	Gly	Gly	Gly	Thr	Cys	Cys	Thr	Gly	Ala	Gly
2180						2185					2190			
Gly	Ala	Gly	Cys	Ala	Gly	Thr	Thr	Cys	Ala	Cys	Ala	Gly	Thr	Gly
2195						2200					2205			
Thr	Thr	Gly	Thr	Cys	Cys	Cys	Thr	Cys	Thr	Cys	Ala	Gly	Cys	Thr
2210						2215					2220			
Gly	Gly	Gly	Cys	Gly	Gly	Cys	Cys	Cys	Ala	Ala	Gly	Cys	Gly	Thr
2225						2230					2235			
Cys	Cys	Cys	Cys	Ala	Thr	Gly	Cys	Cys	Cys	Gly	Cys	Cys	Gly	Thr
2240						2245					2250			
Gly	Cys	Gly	Cys	Thr	Cys	Thr	Gly	Cys	Cys	Thr	Gly	Cys	Thr	Gly
2255						2260					2265			
Cys	Thr	Gly	Gly	Gly	Gly	Cys	Cys	Thr	Gly	Ala	Cys	Thr	Thr	Cys
2270						2275					2280			
Thr	Thr	Cys	Ala	Cys	Ala	Gly	Ala	Cys	Gly	Thr	Cys	Ala	Thr	Cys
2285						2290					2295			

Ala Cys Cys Ala Thr Cys Gly Ala Ala Ala Cys Gly Gly Cys Gly
 2300 2305 2310

Gly Ala Thr Cys Ala Thr Gly Cys Cys Ala Gly Gly Cys Thr Gly
 2315 2320 2325

Cys Ala Ala Cys Thr Gly Cys Ala Gly Cys Thr Gly Gly Cys Cys
 2330 2335 2340

Thr Ala Cys Ala Ala Cys Thr Gly Gly Cys Ala Cys Thr Thr Thr
 2345 2350 2355

Gly Ala Gly Gly Thr Gly Ala Ala Thr Gly Ala Cys Cys Gly Gly
 2360 2365 2370

Ala Ala Gly Gly Ala Cys Cys Cys Cys Cys Ala Ala Gly Ala Gly
 2375 2380 2385

Ala Cys Gly Gly Cys Cys Ala Ala Gly Cys Thr Cys Thr Thr Thr
 2390 2395 2400

Thr Cys Ala Gly Thr Gly Cys Cys Ala Gly Ala Cys Thr Thr Thr
 2405 2410 2415

Gly Thr Ala Gly Gly Thr Gly Ala Thr Gly Cys Cys Thr Gly Cys
 2420 2425 2430

Ala Ala Ala Gly Cys Cys Ala Thr Cys Gly Cys Ala Thr Cys Cys
 2435 2440 2445

Cys Gly Gly Gly Thr Gly Cys Gly Gly Gly Gly Gly Gly Cys Cys
 2450 2455 2460

Gly Thr Gly Gly Cys Cys Thr Cys Thr Gly Thr Cys Ala Cys Thr
 2465 2470 2475

Thr Thr Cys Gly Ala Thr Gly Ala Cys Thr Thr Cys Cys Ala Thr
 2480 2485 2490

Ala Ala Gly Ala Ala Cys Thr Cys Ala Gly Cys Cys Cys Gly Cys
 2495 2500 2505

Ala Thr Cys Ala Thr Thr Cys Gly Cys Ala Cys Thr Gly Cys Thr

2510		2515		2520
Gly Thr Cys Thr Thr Thr	Gly Gly Cys Thr Thr Thr	Gly Ala Gly		
2525	2530	2535		
Ala Cys Cys Thr Cys Gly	Gly Ala Ala Gly Cys Gly	Ala Ala Gly		
2540	2545	2550		
Gly Gly Cys Cys Cys Cys	Gly Ala Thr Gly Gly Cys	Ala Thr Gly		
2555	2560	2565		
Gly Cys Cys Cys Thr Gly	Cys Cys Ala Gly Gly	Cys Cys Cys		
2570	2575	2580		
Cys Gly Gly Gly Ala Cys	Cys Ala Gly Gly Cys Thr	Gly Thr Cys		
2585	2590	2595		
Thr Thr Cys Cys Cys Cys	Cys Ala Ala Ala Ala Cys	Gly Gly Gly		
2600	2605	2610		
Cys Thr Gly Gly Thr Gly	Gly Thr Cys Ala Gly Cys	Ala Gly Thr		
2615	2620	2625		
Gly Thr Gly Gly Ala Cys	Gly Thr Gly Cys Ala Gly	Thr Cys Ala		
2630	2635	2640		
Gly Thr Gly Gly Ala Gly	Cys Cys Thr Gly Thr Gly	Gly Ala Thr		
2645	2650	2655		
Cys Ala Gly Ala Gly Gly	Ala Cys Cys Cys Gly Gly	Gly Ala Cys		
2660	2665	2670		
Gly Cys Cys Cys Thr Gly	Cys Ala Ala Cys Gly Cys	Ala Gly Cys		
2675	2680	2685		
Gly Thr Cys Cys Ala Gly	Cys Thr Gly Gly Cys Cys	Ala Thr Cys		
2690	2695	2700		
Gly Ala Gly Ala Thr Cys	Ala Cys Cys Ala Cys Cys	Ala Ala Cys		
2705	2710	2715		
Thr Cys Cys Cys Ala Gly	Gly Ala Ala Gly Cys Gly	Gly Cys Gly		
2720	2725	2730		

Gly Cys Cys Ala Ala Gly Cys Ala Thr Gly Ala Gly Gly Cys Thr
 2735 2740 2745

Cys Ala Gly Ala Gly Ala Cys Thr Gly Gly Ala Gly Cys Ala Gly
 2750 2755 2760

Gly Ala Ala Gly Cys Cys Cys Gly Cys Gly Gly Cys Cys Gly Gly
 2765 2770 2775

Cys Thr Thr Gly Ala Gly Cys Gly Gly Cys Ala Gly Ala Ala Gly
 2780 2785 2790

Ala Thr Cys Cys Thr Gly Gly Ala Cys Cys Ala Gly Thr Cys Ala
 2795 2800 2805

Gly Ala Ala Gly Cys Cys Gly Ala Gly Ala Ala Ala Gly Cys Thr
 2810 2815 2820

Cys Gly Cys Ala Ala Gly Gly Ala Ala Cys Thr Thr Thr Thr Gly
 2825 2830 2835

Gly Ala Gly Cys Thr Gly Gly Ala Gly Gly Cys Thr Cys Thr Gly
 2840 2845 2850

Ala Gly Cys Ala Thr Gly Gly Cys Cys Gly Thr Gly Gly Ala Gly
 2855 2860 2865

Ala Gly Cys Ala Cys Cys Gly Gly Gly Ala Cys Thr Gly Cys Cys
 2870 2875 2880

Ala Ala Gly Gly Cys Gly Gly Ala Gly Gly Cys Cys Gly Ala Gly
 2885 2890 2895

Thr Cys Cys Cys Gly Thr Gly Cys Gly Gly Ala Gly Gly Cys Ala
 2900 2905 2910

Gly Cys Cys Cys Gly Gly Ala Thr Thr Gly Ala Gly Gly Gly Ala
 2915 2920 2925

Gly Ala Ala Gly Gly Gly Thr Cys Cys Gly Thr Gly Cys Thr Gly
 2930 2935 2940

Cys Ala Gly Gly Cys Cys Ala Ala Gly Cys Thr Ala Ala Ala Ala
 2945 2950 2955

Gly Cys Ala Cys Ala Gly Gly Cys Cys Thr Thr Gly Gly Cys Cys
 2960 2965 2970
 Ala Thr Thr Gly Ala Ala Ala Cys Gly Gly Ala Gly Gly Cys Thr
 2975 2980 2985
 Gly Ala Gly Cys Thr Cys Cys Ala Gly Ala Gly Gly Gly Thr Cys
 2990 2995 3000
 Cys Ala Gly Ala Ala Gly Gly Thr Cys Cys Gly Ala Gly Ala Gly
 3005 3010 3015
 Cys Thr Gly Gly Ala Ala Cys Thr Gly Gly Thr Cys Thr Ala Thr
 3020 3025 3030
 Gly Cys Cys Cys Gly Gly Gly Cys Cys Cys Ala Gly Cys Thr Gly
 3035 3040 3045
 Gly Ala Gly Cys Thr Gly Gly Ala Gly Gly Thr Gly Ala Gly Cys
 3050 3055 3060
 Ala Ala Gly Gly Cys Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly
 3065 3070 3075
 Gly Cys Thr Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Thr Gly
 3080 3085 3090
 Ala Ala Gly Ala Ala Gly Thr Thr Cys Ala Ala Gly Cys Ala Gly
 3095 3100 3105
 Ala Thr Gly Ala Cys Ala Gly Ala Gly Gly Cys Cys Ala Thr Ala
 3110 3115 3120
 Gly Gly Cys Cys Cys Cys Ala Gly Cys Ala Cys Cys Ala Thr Cys
 3125 3130 3135
 Ala Gly Gly Gly Ala Cys Cys Thr Thr Gly Cys Thr Gly Thr Gly
 3140 3145 3150
 Gly Cys Thr Gly Gly Gly Cys Cys Thr Gly Ala Gly Ala Thr Gly
 3155 3160 3165
 Cys Ala Gly Gly Thr Ala Ala Ala Ala Cys Thr Gly Cys Thr Cys

3170		3175		3180
Cys Ala Gly Thr Cys Cys Cys Thr Gly Gly Gly Cys Cys Thr Gly				
3185		3190		3195
Ala Ala Ala Thr Cys Ala Ala Cys Cys Cys Thr Cys Ala Thr Cys				
3200		3205		3210
Ala Cys Cys Gly Ala Thr Gly Gly Cys Thr Cys Cys Ala Cys Thr				
3215		3220		3225
Cys Cys Cys Ala Thr Cys Ala Ala Cys Cys Thr Cys Thr Thr Cys				
3230		3235		3240
Ala Ala Cys Ala Cys Ala Gly Cys Cys Thr Thr Thr Gly Gly Gly				
3245		3250		3255
Cys Thr Gly Cys Thr Gly Gly Gly Gly Ala Thr Gly Gly Gly Gly				
3260		3265		3270
Cys Cys Cys Gly Ala Gly Gly Gly Thr Cys Ala Gly Cys Cys Cys				
3275		3280		3285
Cys Thr Gly Gly Gly Cys Ala Gly Ala Ala Gly Gly Gly Thr Gly				
3290		3295		3300
Gly Cys Cys Ala Gly Thr Gly Gly Gly Cys Cys Cys Ala Gly Cys				
3305		3310		3315
Cys Cys Thr Gly Gly Gly Gly Ala Gly Gly Gly Gly Ala Thr Ala				
3320		3325		3330
Thr Cys Cys Cys Cys Cys Cys Ala Gly Thr Cys Thr Gly Cys Thr				
3335		3340		3345
Cys Ala Gly Gly Cys Cys Cys Cys Thr Cys Ala Ala Gly Cys Thr				
3350		3355		3360
Cys Cys Thr Gly Gly Ala Gly Ala Cys Ala Ala Cys Cys Ala Cys				
3365		3370		3375
Gly Thr Gly Gly Thr Gly Cys Cys Thr Gly Thr Ala Cys Thr Gly				
3380		3385		3390

Cys Gly Cys Thr Ala Ala
3395

<210> 48
<211> 1100
<212> PRT
<213> Artificial Sequence

<220>
<223> synthesized and Rattus norvegicus

<400> 48

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Met
 225 230 235 240

Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile His
 245 250 255

Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys
 260 265 270

Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val Arg
 275 280 285

Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro Val
 290 295 300

Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln Val
 305 310 315 320

Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro Phe
 325 330 335

Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln
 340 345 350

Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe
 355 360 365

Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu Phe
 370 375 380

Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val Glu
 385 390 395 400

Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu Arg
 405 410 415

Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr Gly
 420 425 430

Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val Phe
 435 440 445

Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr
 450 455 460

Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly Val
 465 470 475 480

Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu
 485 490 495

Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro Ile
 500 505 510

Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met Gly
 515 520 525

Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu
 530 535 540

Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile Gln
 545 550 555 560

Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala Leu
 565 570 575

Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln Ala
 580 585 590

Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala
 595 600 605

Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln Asn
 610 615 620

Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val
 625 630 635 640

Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys

645	650	655
Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp Pro 660 665 670		
Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro Ser 675 680 685		
Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn 690 695 700		
Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val Val 705 710 715 720		
Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr Val 725 730 735		
Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala 740 745 750		
Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile 755 760 765		
Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp 770 775 780		
His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys Leu 785 790 795 800		
Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser 805 810 815		
Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys 820 825 830		
Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met Ser 835 840 845		
Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp Gln 850 855 860		
Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln 865 870 875 880		

Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser
 885 890 895

Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala
 900 905 910

Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu
 915 920 925

Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu
 930 935 940

Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly Asn
 945 950 955 960

Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly
 965 970 975

Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile
 980 985 990

Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met Glu
 995 1000 1005

Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 1010 1015 1020

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr
 1025 1030 1035

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly
 1040 1045 1050

Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
 1055 1060 1065

Thr Leu Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr
 1070 1075 1080

Ala Phe Gly Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala
 1085 1090 1095

Gln Lys
 1100

<210> 49
 <211> 3303
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 49

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Ala Ala Cys Thr Gly Thr Thr Cys Ala Cys Thr Gly Gly Cys Gly Thr
 20 25 30

Gly Gly Thr Cys Cys Cys Ala Ala Thr Thr Cys Thr Cys Gly Thr Gly
 35 40 45

Gly Ala Ala Cys Thr Gly Gly Ala Thr Gly Gly Cys Gly Ala Thr Gly
 50 55 60

Thr Gly Ala Ala Thr Gly Gly Gly Cys Ala Cys Ala Ala Ala Thr Thr
 65 70 75 80

Thr Thr Cys Thr Gly Thr Cys Ala Gly Cys Gly Gly Ala Gly Ala Gly
 85 90 95

Gly Gly Thr Gly Ala Ala Gly Gly Thr Gly Ala Thr Gly Cys Cys Ala
 100 105 110

Cys Ala Thr Ala Cys Gly Gly Ala Ala Ala Gly Cys Thr Cys Ala Cys
 115 120 125

Cys Cys Thr Gly Ala Ala Ala Thr Thr Cys Ala Thr Cys Thr Gly Cys
 130 135 140

Ala Cys Cys Ala Cys Thr Gly Gly Ala Ala Ala Gly Cys Thr Cys Cys
 145 150 155 160

Cys Thr Gly Thr Gly Cys Cys Ala Thr Gly Gly Cys Cys Ala Ala Cys
 165 170 175

Ala Cys Thr Gly Gly Thr Cys Ala Cys Thr Ala Cys Cys Thr Thr Cys
 180 185 190

Ala Cys Cys Thr Ala Thr Gly Gly Cys Gly Thr Gly Cys Ala Gly Thr
 195 200 205

Gly Cys Thr Thr Thr Thr Cys Cys Ala Gly Ala Thr Ala Cys Cys Cys
 210 215 220

Ala Gly Ala Cys Cys Ala Thr Ala Thr Gly Ala Ala Gly Cys Ala Gly
 225 230 235 240

Cys Ala Thr Gly Ala Cys Thr Thr Thr Thr Thr Cys Ala Ala Gly Ala
 245 250 255

Gly Cys Gly Cys Cys Ala Thr Gly Cys Cys Cys Gly Ala Gly Gly Gly
 260 265 270

Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Gly Ala Gly Ala
 275 280 285

Ala Cys Cys Ala Thr Cys Thr Thr Thr Thr Thr Cys Ala Ala Ala Gly
 290 295 300

Ala Thr Gly Ala Cys Gly Gly Gly Ala Ala Cys Thr Ala Cys Ala Ala
 305 310 315 320

Gly Ala Cys Cys Cys Gly Cys Gly Cys Thr Gly Ala Ala Gly Thr Cys
 325 330 335

Ala Ala Gly Thr Thr Cys Gly Ala Ala Gly Gly Thr Gly Ala Cys Ala
 340 345 350

Cys Cys Cys Thr Gly Gly Thr Gly Ala Ala Thr Ala Gly Ala Ala Thr
 355 360 365

Cys Gly Ala Gly Cys Thr Gly Ala Ala Gly Gly Gly Cys Ala Thr Thr
 370 375 380

Gly Ala Cys Thr Thr Thr Ala Ala Gly Gly Ala Gly Gly Ala Thr Gly
 385 390 395 400

Gly Ala Ala Ala Cys Ala Thr Thr Cys Thr Cys Gly Gly Cys Cys Ala
 405 410 415

Cys Ala Ala Gly Cys Thr Gly Gly Ala Ala Thr Ala Cys Ala Ala Cys
 420 425 430

Thr Ala Thr Ala Ala Cys Thr Cys Cys Cys Ala Cys Ala Ala Thr Gly
 435 440 445

Thr Gly Thr Ala Cys Ala Thr Cys Ala Thr Gly Gly Cys Cys Gly Ala
 450 455 460

Cys Ala Ala Gly Cys Ala Ala Ala Ala Gly Ala Ala Thr Gly Gly Cys
 465 470 475 480

Ala Thr Cys Ala Ala Gly Gly Thr Cys Ala Ala Cys Thr Thr Cys Ala
 485 490 495

Ala Gly Ala Thr Cys Ala Gly Ala Cys Ala Cys Ala Ala Cys Ala Thr
 500 505 510

Thr Gly Ala Gly Gly Ala Thr Gly Gly Ala Thr Cys Cys Gly Thr Gly
 515 520 525

Cys Ala Gly Cys Thr Gly Gly Cys Cys Gly Ala Cys Cys Ala Thr Thr
 530 535 540

Ala Thr Cys Ala Ala Cys Ala Gly Ala Ala Cys Ala Cys Thr Cys Cys
 545 550 555 560

Ala Ala Thr Cys Gly Gly Cys Gly Ala Cys Gly Gly Cys Cys Cys Thr
 565 570 575

Gly Thr Gly Cys Thr Cys Cys Thr Cys Cys Cys Ala Gly Ala Cys Ala
 580 585 590

Ala Cys Cys Ala Thr Thr Ala Cys Cys Thr Gly Thr Cys Cys Ala Cys
 595 600 605

Cys Cys Ala Gly Thr Cys Thr Gly Cys Cys Cys Thr Gly Thr Cys Thr
 610 615 620

Ala Ala Ala Gly Ala Thr Cys Cys Cys Ala Ala Cys Gly Ala Ala Ala
 625 630 635 640

Ala Gly Ala Gly Ala Gly Ala Cys Cys Ala Cys Ala Thr Gly Gly Thr
 645 650 655

Cys Cys Thr Gly Cys Thr Gly Gly Ala Gly Thr Thr Thr Gly Thr Gly

660	665	670
Ala Cys Cys Gly Cys Thr Gly Cys Thr Gly Gly Gly Ala Thr Cys Ala		
675	680	685
Cys Ala Cys Ala Thr Gly Gly Cys Ala Thr Gly Gly Ala Cys Gly Ala		
690	695	700
Gly Cys Thr Gly Thr Ala Cys Ala Ala Gly Cys Cys Cys Ala Thr Gly		
705	710	715
Gly Cys Ala Ala Cys Thr Gly Ala Ala Gly Ala Gly Gly Cys Cys Ala		
725	730	735
Thr Cys Ala Thr Cys Cys Gly Cys Ala Thr Cys Cys Cys Cys Cys Cys		
740	745	750
Ala Thr Ala Cys Cys Ala Cys Thr Ala Cys Ala Thr Cys Cys Ala Thr		
755	760	765
Gly Thr Gly Cys Thr Gly Gly Ala Cys Cys Ala Gly Ala Ala Cys Ala		
770	775	780
Gly Thr Ala Ala Thr Gly Thr Gly Thr Cys Cys Cys Gly Thr Gly Thr		
785	790	795
Gly Gly Ala Gly Gly Thr Thr Gly Gly Ala Cys Cys Ala Ala Ala Gly		
805	810	815
Ala Cys Cys Thr Ala Cys Ala Thr Cys Cys Gly Gly Cys Ala Gly Gly		
820	825	830
Ala Cys Ala Ala Thr Gly Ala Gly Ala Gly Gly Gly Thr Ala Cys Thr		
835	840	845
Gly Thr Thr Thr Gly Cys Cys Cys Cys Ala Gly Thr Thr Cys Gly Cys		
850	855	860
Ala Thr Gly Gly Thr Gly Ala Cys Cys Gly Thr Cys Cys Cys Cys Cys		
865	870	875
Cys Ala Cys Gly Cys Cys Ala Cys Thr Ala Cys Thr Gly Cys Ala Thr		
885	890	895

Ala Gly Thr Gly Gly Cys Cys Ala Ala Cys Cys Cys Thr Gly Thr Gly
 900 905 910

Thr Cys Cys Cys Gly Gly Gly Ala Cys Ala Cys Cys Cys Ala Gly Ala
 915 920 925

Gly Thr Thr Cys Thr Gly Thr Gly Thr Thr Ala Thr Thr Thr Gly Ala
 930 935 940

Cys Ala Thr Cys Ala Cys Ala Gly Gly Ala Cys Ala Ala Gly Thr Cys
 945 950 955 960

Cys Gly Ala Cys Thr Cys Cys Gly Gly Cys Ala Cys Gly Cys Thr Gly
 965 970 975

Ala Cys Cys Ala Gly Gly Ala Gly Ala Thr Cys Cys Gly Ala Cys Thr
 980 985 990

Ala Gly Cys Cys Cys Ala Gly Gly Ala Cys Cys Cys Cys Thr Thr Cys
 995 1000 1005

Cys Cys Cys Cys Thr Gly Thr Ala Thr Cys Cys Ala Gly Gly Gly
 1010 1015 1020

Gly Ala Gly Gly Thr Gly Cys Thr Gly Gly Ala Ala Ala Ala Gly
 1025 1030 1035

Gly Ala Cys Ala Thr Cys Ala Cys Cys Cys Cys Ala Cys Thr Gly
 1040 1045 1050

Cys Ala Gly Gly Thr Gly Gly Thr Thr Cys Thr Gly Cys Cys Cys
 1055 1060 1065

Ala Ala Cys Ala Cys Ala Gly Cys Ala Cys Thr Gly Cys Ala Thr
 1070 1075 1080

Cys Thr Thr Ala Ala Gly Gly Cys Gly Thr Thr Gly Cys Thr Gly
 1085 1090 1095

Gly Ala Cys Thr Thr Thr Gly Ala Gly Gly Ala Thr Ala Ala Gly
 1100 1105 1110

Ala Ala Thr Gly Gly Ala Gly Ala Cys Ala Ala Gly Gly Thr Cys
 1115 1120 1125

Ala Thr Gly Gly Cys Ala Gly Gly Ala Gly Ala Cys Gly Ala Gly	1130	1135	1140
Thr Gly Gly Cys Thr Ala Thr Thr Thr Gly Ala Gly Gly Gly Ala	1145	1150	1155
Cys Cys Thr Gly Gly Cys Ala Cys Cys Thr Ala Cys Ala Thr Cys	1160	1165	1170
Cys Cys Ala Cys Ala Gly Ala Ala Gly Gly Ala Ala Gly Thr Gly	1175	1180	1185
Gly Ala Ala Gly Thr Cys Gly Thr Gly Gly Ala Gly Ala Thr Cys	1190	1195	1200
Ala Thr Thr Cys Ala Gly Gly Cys Cys Ala Cys Ala Gly Thr Cys	1205	1210	1215
Ala Thr Cys Ala Ala Ala Cys Ala Gly Ala Ala Cys Cys Ala Ala	1220	1225	1230
Gly Cys Ala Cys Thr Gly Cys Gly Gly Cys Thr Ala Ala Gly Gly	1235	1240	1245
Gly Cys Cys Cys Gly Ala Ala Ala Gly Gly Ala Gly Thr Gly Cys	1250	1255	1260
Thr Thr Thr Gly Ala Cys Cys Gly Gly Gly Ala Gly Gly Gly Cys	1265	1270	1275
Ala Ala Gly Gly Gly Gly Cys Gly Cys Gly Thr Gly Ala Cys Ala	1280	1285	1290
Gly Gly Thr Gly Ala Gly Gly Ala Gly Thr Gly Gly Cys Thr Gly	1295	1300	1305
Gly Thr Cys Cys Gly Ala Thr Cys Cys Gly Thr Gly Gly Gly Gly	1310	1315	1320
Gly Cys Thr Thr Ala Cys Cys Thr Cys Cys Cys Ala Gly Cys Thr	1325	1330	1335
Gly Thr Cys Thr Thr Thr Gly Ala Ala Gly Ala Gly Gly Thr Gly			

1340	1345	1350
Cys Thr Gly Gly Ala Thr	Cys Thr Gly Gly Thr	Gly Gly Ala Thr
1355	1360	1365
Gly Cys Thr Gly Thr Gly Ala	Thr Cys Cys Thr Thr	Ala Cys Ala
1370	1375	1380
Gly Ala Ala Ala Ala Gly Ala	Cys Thr Gly Cys Cys	Cys Thr Gly
1385	1390	1395
Cys Ala Cys Cys Thr Cys Cys	Gly Gly Gly Cys Thr	Cys Thr Gly
1400	1405	1410
Cys Ala Gly Ala Ala Cys Thr	Thr Cys Ala Gly Gly	Gly Ala Cys
1415	1420	1425
Cys Thr Thr Cys Gly Gly Gly	Gly Ala Gly Thr Gly	Cys Thr Cys
1430	1435	1440
Cys Ala Cys Cys Gly Cys Ala	Cys Cys Gly Gly Gly	Gly Ala Gly
1445	1450	1455
Gly Ala Ala Thr Gly Gly Thr	Thr Ala Gly Thr Gly	Ala Cys Ala
1460	1465	1470
Gly Thr Gly Cys Ala Gly Gly	Ala Cys Ala Cys Ala	Gly Ala Ala
1475	1480	1485
Gly Cys Cys Cys Ala Thr Gly	Thr Thr Cys Cys Ala	Gly Ala Thr
1490	1495	1500
Gly Thr Cys Thr Ala Thr Gly	Ala Gly Gly Ala Gly	Gly Thr Gly
1505	1510	1515
Cys Thr Thr Gly Gly Gly Gly	Thr Ala Gly Thr Ala	Cys Cys Cys
1520	1525	1530
Ala Thr Cys Ala Cys Cys Ala	Cys Cys Cys Thr Gly	Gly Gly Ala
1535	1540	1545
Cys Cys Thr Cys Gly Ala Cys	Ala Cys Thr Ala Cys	Thr Gly Thr
1550	1555	1560

Gly Thr Cys Ala Thr Thr Cys Thr Thr Gly Ala Cys Cys Cys Ala
 1565 1570 1575

Ala Thr Gly Gly Gly Ala Cys Cys Ala Gly Ala Cys Gly Gly Cys
 1580 1585 1590

Ala Ala Gly Ala Ala Cys Cys Ala Gly Cys Thr Gly Gly Gly Ala
 1595 1600 1605

Cys Ala Ala Ala Ala Gly Cys Gly Thr Gly Thr Thr Gly Thr Cys
 1610 1615 1620

Ala Ala Gly Gly Gly Ala Gly Ala Gly Ala Ala Gly Thr Cys Cys
 1625 1630 1635

Thr Thr Thr Thr Thr Cys Cys Thr Cys Cys Ala Gly Cys Cys Ala
 1640 1645 1650

Gly Gly Ala Gly Ala Gly Ala Gly Gly Cys Thr Gly Gly Ala Gly
 1655 1660 1665

Cys Gly Ala Gly Gly Cys Ala Thr Cys Cys Ala Gly Gly Ala Thr
 1670 1675 1680

Gly Thr Gly Thr Ala Thr Gly Thr Gly Cys Thr Gly Thr Cys Ala
 1685 1690 1695

Gly Ala Gly Cys Ala Gly Cys Ala Gly Gly Gly Gly Cys Thr Gly
 1700 1705 1710

Cys Thr Ala Cys Thr Gly Ala Ala Gly Gly Cys Ala Cys Thr Gly
 1715 1720 1725

Cys Ala Gly Cys Cys Cys Cys Thr Gly Gly Ala Gly Gly Ala Gly
 1730 1735 1740

Gly Gly Ala Gly Ala Gly Ala Gly Cys Gly Ala Gly Gly Ala Gly
 1745 1750 1755

Ala Ala Gly Gly Thr Cys Thr Cys Cys Cys Ala Thr Cys Ala Gly
 1760 1765 1770

Gly Cys Cys Gly Gly Ala Gly Ala Cys Thr Gly Cys Thr Gly Gly
 1775 1780 1785

Cys	Thr	Cys	Ala	Thr	Cys	Cys	Gly	Thr	Gly	Gly	Gly	Cys	Cys	Cys
1790						1795					1800			
Cys	Thr	Gly	Gly	Ala	Gly	Thr	Ala	Thr	Gly	Thr	Gly	Cys	Cys	Ala
1805						1810					1815			
Thr	Cys	Thr	Gly	Cys	Ala	Ala	Ala	Ala	Gly	Thr	Gly	Gly	Ala	Gly
1820						1825					1830			
Gly	Thr	Gly	Gly	Thr	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Cys	Gly	Thr
1835						1840					1845			
Cys	Ala	Gly	Gly	Cys	Thr	Ala	Thr	Cys	Cys	Cys	Thr	Cys	Thr	Gly
1850						1855					1860			
Gly	Ala	Cys	Cys	Ala	Ala	Ala	Ala	Thr	Gly	Ala	Gly	Gly	Gly	Cys
1865						1870					1875			
Ala	Thr	Cys	Thr	Ala	Thr	Gly	Thr	Gly	Cys	Ala	Gly	Gly	Ala	Thr
1880						1885					1890			
Gly	Thr	Cys	Ala	Ala	Gly	Ala	Cys	Gly	Gly	Gly	Gly	Ala	Ala	Gly
1895						1900					1905			
Gly	Thr	Gly	Cys	Gly	Gly	Gly	Cys	Thr	Gly	Thr	Gly	Ala	Thr	Thr
1910						1915					1920			
Gly	Gly	Ala	Ala	Gly	Cys	Ala	Cys	Cys	Thr	Ala	Cys	Ala	Thr	Gly
1925						1930					1935			
Cys	Thr	Gly	Ala	Cys	Thr	Cys	Ala	Gly	Gly	Ala	Thr	Gly	Ala	Ala
1940						1945					1950			
Gly	Thr	Cys	Cys	Thr	Gly	Thr	Gly	Gly	Gly	Ala	Ala	Ala	Ala	Gly
1955						1960					1965			
Gly	Ala	Gly	Cys	Thr	Gly	Cys	Cys	Thr	Thr	Cys	Thr	Gly	Gly	Gly
1970						1975					1980			
Gly	Thr	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Cys	Thr	Gly	Cys	Thr	Gly
1985						1990					1995			
Ala	Ala	Cys	Thr	Thr	Gly	Gly	Gly	Gly	Cys	Ala	Thr	Gly	Ala	Cys

2000	2005	2010
Cys Cys Thr Cys Thr Gly Gly 2015	Cys Ala Gly Ala Cys 2020	Ala Gly Gly 2025
Gly Gly Thr Cys Ala Gly Ala 2030	Ala Gly Gly Gly Cys 2035	Ala Cys Ala 2040
Gly Cys Cys Ala Ala Gly Cys 2045	Cys Cys Cys Thr Thr 2050	Cys Ala Gly 2055
Cys Cys Cys Thr Cys Ala Gly 2060	Cys Thr Cys Cys Ala 2065	Ala Gly Gly 2070
Ala Ala Cys Ala Ala Gly Ala 2075	Cys Cys Cys Gly Ala 2080	Gly Thr Gly 2085
Gly Thr Cys Ala Gly Cys Thr 2090	Ala Cys Cys Gly Thr 2095	Gly Thr Cys 2100
Cys Cys Gly Cys Ala Cys Ala 2105	Ala Thr Gly Cys Ala 2110	Gly Cys Gly 2115
Gly Thr Gly Cys Ala Gly Gly 2120	Thr Cys Thr Ala Thr 2125	Gly Ala Cys 2130
Thr Ala Cys Ala Gly Ala Gly 2135	Cys Cys Ala Ala Gly 2140	Ala Gly Ala 2145
Gly Cys Cys Cys Gly Thr Gly 2150	Thr Gly Gly Thr Cys 2155	Thr Thr Thr 2160
Gly Gly Gly Cys Cys Cys Gly 2165	Ala Gly Cys Thr Ala 2170	Gly Thr Gly 2175
Ala Cys Ala Cys Thr Gly Gly 2180	Ala Thr Cys Cys Thr 2185	Gly Ala Gly 2190
Gly Ala Gly Cys Ala Gly Thr 2195	Thr Cys Ala Cys Ala 2200	Gly Thr Ala 2205
Thr Thr Gly Thr Cys Cys Cys 2210	Thr Thr Thr Cys Thr 2215	Gly Cys Cys 2220

Gly Gly Gly Cys Gly Ala Cys Cys Cys Ala Ala Gly Cys Gly Thr
 2225 2230 2235

Cys Cys Thr Cys Ala Thr Gly Cys Cys Cys Gly Cys Cys Gly Thr
 2240 2245 2250

Gly Cys Ala Cys Thr Cys Thr Gly Cys Cys Thr Ala Cys Thr Gly
 2255 2260 2265

Cys Thr Gly Gly Gly Ala Cys Cys Thr Gly Ala Thr Thr Thr Cys
 2270 2275 2280

Thr Thr Thr Ala Cys Thr Gly Ala Thr Gly Thr Cys Ala Thr Cys
 2285 2290 2295

Ala Cys Cys Ala Thr Cys Gly Ala Ala Ala Cys Thr Gly Cys Ala
 2300 2305 2310

Gly Ala Thr Cys Ala Thr Gly Cys Cys Ala Gly Gly Thr Thr Gly
 2315 2320 2325

Cys Ala Gly Cys Thr Gly Cys Ala Gly Cys Thr Thr Gly Cys Cys
 2330 2335 2340

Thr Ala Cys Ala Ala Cys Thr Gly Gly Cys Ala Cys Thr Thr Thr
 2345 2350 2355

Gly Ala Ala Cys Thr Gly Ala Ala Gly Ala Ala Cys Cys Gly Gly
 2360 2365 2370

Ala Ala Thr Gly Ala Cys Cys Cys Thr Gly Cys Ala Gly Ala Gly
 2375 2380 2385

Gly Cys Ala Gly Cys Cys Ala Ala Gly Cys Thr Thr Thr Thr Cys
 2390 2395 2400

Thr Cys Cys Gly Thr Gly Cys Cys Thr Gly Ala Cys Thr Thr Cys
 2405 2410 2415

Gly Thr Gly Gly Gly Thr Gly Ala Cys Gly Cys Cys Thr Gly Cys
 2420 2425 2430

Ala Ala Gly Gly Cys Cys Ala Thr Thr Gly Cys Ala Thr Cys Cys
 2435 2440 2445

Cys Gly Ala Gly Thr Cys Cys Gly Gly Gly Gly Gly Gly Cys Thr
 2450 2455 2460

Gly Thr Ala Gly Cys Cys Thr Cys Thr Gly Thr Cys Ala Cys Cys
 2465 2470 2475

Thr Thr Thr Gly Ala Thr Gly Ala Cys Thr Thr Cys Cys Ala Thr
 2480 2485 2490

Ala Ala Ala Ala Ala Cys Thr Cys Ala Gly Cys Cys Cys Gly Gly
 2495 2500 2505

Ala Thr Cys Ala Thr Thr Cys Gly Ala Ala Thr Gly Gly Cys Thr
 2510 2515 2520

Gly Thr Thr Thr Thr Thr Gly Gly Cys Thr Thr Thr Gly Ala Gly
 2525 2530 2535

Ala Thr Gly Thr Cys Thr Gly Ala Ala Gly Ala Cys Ala Cys Ala
 2540 2545 2550

Gly Gly Thr Cys Cys Thr Gly Ala Thr Gly Gly Cys Ala Cys Ala
 2555 2560 2565

Cys Thr Cys Cys Thr Gly Cys Cys Cys Ala Ala Gly Gly Cys Thr
 2570 2575 2580

Cys Gly Ala Gly Ala Cys Cys Ala Gly Gly Cys Ala Gly Thr Cys
 2585 2590 2595

Thr Thr Thr Cys Cys Cys Cys Ala Ala Ala Ala Cys Gly Gly Gly
 2600 2605 2610

Cys Thr Gly Gly Thr Ala Gly Thr Cys Ala Gly Cys Ala Gly Thr
 2615 2620 2625

Gly Thr Gly Gly Ala Thr Gly Thr Gly Cys Ala Gly Thr Cys Ala
 2630 2635 2640

Gly Thr Gly Gly Ala Gly Cys Cys Cys Gly Thr Gly Gly Ala Cys
 2645 2650 2655

Cys Ala Gly Ala Gly Gly Ala Cys Cys Cys Gly Gly Gly Ala Thr

2660	2665	2670
Gly Cys Cys Cys Thr Thr Cys Ala Gly Cys Gly Cys Ala Gly Cys		
2675	2680	2685
Gly Thr Thr Cys Ala Gly Cys Thr Gly Gly Cys Cys Ala Thr Cys		
2690	2695	2700
Gly Ala Ala Ala Thr Thr Ala Cys Cys Ala Cys Cys Ala Ala Cys		
2705	2710	2715
Thr Cys Cys Cys Ala Gly Gly Ala Gly Gly Cys Ala Gly Cys Ala		
2720	2725	2730
Gly Cys Cys Ala Ala Gly Cys Ala Cys Gly Ala Gly Gly Cys Thr		
2735	2740	2745
Cys Ala Gly Ala Gly Ala Cys Thr Gly Gly Ala Ala Cys Ala Gly		
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Gly Ala Ala Gly Cys Cys Cys Gly Thr Gly Gly Thr Cys Gly Gly		
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Cys Thr Thr Gly Ala Gly Ala Gly Gly Cys Ala Gly Ala Ala Gly		
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Ala Thr Cys Thr Thr Gly Gly Ala Cys Cys Ala Gly Thr Cys Ala		
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Gly Ala Ala Gly Cys Thr Gly Ala Ala Ala Ala Ala Gly Cys Cys		
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Cys Gly Cys Ala Ala Gly Gly Ala Ala Cys Thr Cys Thr Thr Gly		
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Gly Ala Gly Cys Thr Thr Gly Ala Gly Gly Cys Thr Ala Thr Gly		
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Ala Gly Cys Ala Thr Gly Gly Cys Thr Gly Thr Gly Gly Ala Gly		
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Ala Gly Cys Ala Cys Gly Gly Gly Thr Ala Ala Thr Gly Cys Cys		
2870	2875	2880

Ala Ala Ala Gly Cys Ala Gly Ala Gly Gly Cys Thr Gly Ala Gly
2885 2890 2895

Thr Cys Cys Cys Gly Thr Gly Cys Ala Gly Ala Gly Gly Cys Ala
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Gly Cys Gly Ala Gly Gly Ala Thr Cys Gly Ala Ala Gly Gly Ala
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Gly Ala Ala Gly Gly Cys Thr Cys Thr Gly Thr Gly Cys Thr Gly
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Cys Ala Gly Gly Cys Cys Ala Ala Gly Cys Thr Cys Ala Ala Gly
2945 2950 2955

Gly Cys Ala Cys Ala Gly Gly Cys Gly Cys Thr Ala Gly Cys Cys
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Ala Thr Thr Gly Ala Gly Ala Cys Gly Gly Ala Gly Gly Cys Thr
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Gly Ala Gly Thr Thr Gly Gly Ala Gly Cys Gly Ala Gly Thr Ala
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Ala Ala Gly Ala Ala Ala Gly Thr Ala Cys Gly Ala Gly Ala Gly
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Gly Ala Gly Cys Thr Gly Gly Ala Gly Gly Thr Gly Ala Gly Cys
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Ala Ala Gly Gly Cys Gly Cys Ala Gly Cys Ala Gly Cys Thr Thr
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Gly Cys Cys Ala Ala Thr Gly Thr Gly Gly Ala Gly Gly Cys Ala
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Ala Ala Gly Ala Ala Gly Thr Thr Cys Ala Ala Gly Gly Ala Gly
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Ala Thr Gly Ala Cys Ala Gly Ala Gly Gly Cys Ala Cys Thr Gly
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Gly Gly Cys Cys Cys Cys Gly Gly Cys Ala Cys Cys Ala Thr Cys
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Ala Gly Gly Gly Ala Cys Cys Thr Gly Gly Cys Thr Gly Thr Gly
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Cys Ala Gly Gly Thr Gly Ala Ala Ala Cys Thr Thr Cys Thr Cys
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Cys Ala Gly Thr Cys Cys Cys Thr Gly Gly Gly Cys Cys Thr Gly
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Ala Cys Cys Gly Ala Thr Gly Gly Cys Thr Cys Gly Thr Cys Thr
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Cys Cys Cys Ala Thr Cys Ala Ala Cys Cys Thr Cys Thr Thr Cys
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Ala Gly Cys Ala Cys Ala Gly Cys Cys Thr Thr Cys Gly Gly Gly
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Thr Thr Gly Cys Thr Gly Gly Gly Gly Cys Thr Gly Gly Gly Gly
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Thr Cys Thr Gly Ala Thr Gly Gly Thr Cys Ala Gly Cys Cys Gly
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<212> PRT

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<223> synthesized and Homo sapiens

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Gln Ser Arg Thr Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser Val
 35 40 45

Gly Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser Ser
 50 55 60

Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys Phe
 65 70 75 80

Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu
 85 90 95

Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln Asp
 100 105 110

Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe
 115 120 125

Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn
 130 135 140

Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln Ser Leu Gly Val
 145 150 155 160

Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr Met Leu Val Leu
 165 170 175

Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile Val Phe Lys Ser
 180 185 190

Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn Ile Pro Trp Ala
 195 200 205

Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg Arg Thr Glu Gly

210

215

220

Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp
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Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln Pro Ile Ser Thr Val Ser
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Pro Leu His Arg Val Leu His Tyr Ser Gln Gly
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<211> 804

<212> DNA

<213> Artificial Sequence

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<400> 51

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 35 40 45

Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr His Ile Ile Leu Asp Asn
 50 55 60

Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn Ser Ile Gln Lys Asn His
 65 70 75 80

Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser Ile Arg Glu Lys
 85 90 95

Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro Tyr Lys Pro Leu Asp Ile
 100 105 110

Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Ser Glu Val Lys Thr Glu
 115 120 125

Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu Glu Asp Thr Val Glu Leu
 130 135 140

Thr Glu Phe Gly Met Gln Asn Val Glu Ile Pro His Leu Pro Gln Asp
 145 150 155 160

Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu Lys Val Gly Met Glu Gly
 165 170 175

Gly Gln Glu Ala Val Val Val Glu Leu Gln Cys Ser Arg Asp Ser Arg
 180 185 190

Asp Cys Pro Phe Leu Ile Ser Ser His Phe Leu Leu Asp Asp Gly Met
 195 200 205

Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys Thr Ser Glu Asp Ala Ser

210	215	220
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Leu Arg Glu His Phe Thr Pro Glu Ala Thr Gln Leu Ala Ser Glu Gln		
	245	250 255
Leu Gln Ala Leu Leu Leu Glu Glu Val Met Asn Ser Ser Thr Leu Ser		
	260	265 270
Gln Glu Val Ser Asp Leu Val Glu Met Ile Trp Ala Glu Ala Leu Gly		
	275	280 285
His Leu Glu His Met Leu Leu Lys Pro Val Asn Arg Ile Ser Leu Asn		
	290	295 300
Asp Val Ser Lys Ala Glu Gly Ile Leu Leu Leu Val Lys Ala Ala Leu		
305	310	315 320
Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln Lys Met Met Thr Glu Phe		
	325	330 335
Tyr Arg Leu Ile Pro His Lys Gly Thr Met Pro Lys Glu Val Asn Leu		
	340	345 350
Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys Gln Leu Ile Arg Asp Met		
	355	360 365
Val Asn Val Cys Glu Thr Asn Leu Ser Lys Pro Asn Pro Pro Ser Leu		
	370	375 380
Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile Glu His Val Glu Gln Asn		
385	390	395 400
Thr Glu Glu Phe Leu Arg Val Arg Lys Glu Val Leu Gln Asn His His		
	405	410 415
Ser Lys Ser Pro Val Asp Val Leu Gln Ile Phe Arg Val Gly Arg Val		
	420	425 430
Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu Gly Asn Val Arg Pro Leu		
	435	440 445

Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile Leu Cys Arg Gly
 450 455 460

Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val Gln Arg Thr Asp
 465 470 475 480

Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe Ser Asp Ser Leu Ser Thr
 485 490 495

Ser Ile Lys Tyr Ser His Pro Gly Glu Thr Asp Gly Thr Arg Leu Leu
 500 505 510

Leu Ile Cys Asp Val Ala Leu Gly Lys Cys Met Asp Leu His Glu Lys
 515 520 525

Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp Ser Val His Gly
 530 535 540

Val Ser Gln Thr Ala Ser Val Thr Thr Asp Phe Glu Asp Asp Glu Phe
 545 550 555 560

Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr Ile Ile Lys Phe
 565 570 575

Ser Met Pro Gly Asp Gln Ile Lys Asp Phe His Pro Ser Asp His Thr
 580 585 590

Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser Asn Phe Ser Lys Val Glu
 595 600 605

Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser Ser Ser Thr Lys Ala Gly
 610 615 620

Leu Gln Asp Ala Ser Gly Asn Leu Val Pro Leu Glu Asp Val His Ile
 625 630 635 640

Lys Gly Arg Ile Ile Asp Thr Val Ala Gln Val Ile Val Phe Gln Thr
 645 650 655

Tyr Thr Asn Lys Ser His Val Pro Ile Glu Ala Lys Tyr Ile Phe Pro
 660 665 670

Leu Asp Asp Lys Ala Ala Val Cys Gly Phe Glu Ala Phe Ile Asn Gly
 675 680 685

Lys His Ile Val Gly Glu Ile Lys Glu Lys Glu Glu Ala Gln Gln Glu
 690 695 700

Tyr Leu Glu Ala Val Thr Gln Gly His Gly Ala Tyr Leu Met Ser Gln
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Asp Ala Pro Asp Val Phe Thr Val Ser Val Gly Asn Leu Pro Pro Lys
 725 730 735

Ala Lys Val Leu Ile Lys Ile Thr Tyr Ile Thr Glu Leu Ser Ile Leu
 740 745 750

Gly Thr Val Gly Val Phe Phe Met Pro Ala Thr Val Ala Pro Trp Gln
 755 760 765

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Cys Ile Lys Glu Ile Gly Thr Lys Gln Ser Phe Ser Leu Thr Met Ser
 785 790 795 800

Ile Glu Met Pro Tyr Val Ile Glu Phe Ile Phe Ser Asp Thr His Glu
 805 810 815

Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala Val Ile Ser Thr Met Glu
 820 825 830

Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser Leu His Ile Gly Leu Ser
 835 840 845

Ala Ala Tyr Leu Pro Arg Met Trp Val Glu Lys His Pro Glu Lys Glu
 850 855 860

Ser Glu Ala Cys Met Leu Val Phe Gln Pro Asp Leu Asp Val Asp Leu
 865 870 875 880

Pro Asp Leu Ala Ser Glu Ser Glu Val Ile Ile Cys Leu Asp Cys Ser
 885 890 895

Ser Ser Met Glu Gly Val Thr Phe Leu Gln Ala Lys Gln Ile Thr Leu
 900 905 910

His Ala Leu Ser Leu Val Gly Glu Lys Gln Lys Val Asn Ile Ile Gln

915	920	925
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Ser Asn Thr Thr Ala Ala Glu Phe Ile Met Ser Ala Thr Pro Thr Met 945 950 955 960		
Gly Asn Thr Asp Phe Trp Lys Thr Leu Arg Tyr Leu Ser Leu Leu Tyr 965 970 975		
Pro Ala Arg Gly Ser Arg Asn Ile Leu Leu Val Ser Asp Gly His Leu 980 985 990		
Gln Asp Glu Ser Leu Thr Leu Gln Leu Val Lys Arg Ser Arg Pro His 995 1000 1005		
Thr Arg Leu Phe Ala Cys Gly Ile Gly Ser Thr Ala Asn Arg His 1010 1015 1020		
Val Leu Arg Ile Leu Ser Gln Cys Gly Ala Gly Val Phe Glu Tyr 1025 1030 1035		
Phe Asn Ala Lys Ser Lys His Ser Trp Arg Lys Gln Ile Glu Asp 1040 1045 1050		
Gln Met Thr Arg Leu Cys Ser Pro Ser Cys His Ser Val Ser Val 1055 1060 1065		
Lys Trp Gln Gln Leu Asn Pro Asp Ala Pro Glu Ala Leu Gln Ala 1070 1075 1080		
Pro Ala Gln Val Pro Ser Leu Phe Arg Asn Asp Arg Leu Leu Val 1085 1090 1095		
Tyr Gly Phe Ile Pro His Cys Thr Gln Ala Thr Leu Cys Ala Leu 1100 1105 1110		
Ile Gln Glu Lys Glu Phe Cys Thr Met Val Ser Thr Thr Glu Leu 1115 1120 1125		
Gln Lys Thr Thr Gly Thr Met Ile His Lys Leu Ala Ala Arg Ala 1130 1135 1140		

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Ala Val	Glu Lys Arg Asp Glu	Asn Glu Ser Pro Phe	Pro Asp Ile
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Pro Lys	Val Ser Glu Leu Ile	Ala Lys Glu Asp Val	Asp Phe Leu
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Pro Tyr	Met Ser Trp Gln Gly	Glu Pro Gln Glu Ala	Val Arg Asn
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Gln Ser	Leu Leu Ala Ser Ser	Glu Trp Pro Glu Leu	Arg Leu Ser
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Lys Arg	Lys His Arg Lys Ile	Pro Phe Ser Lys Arg	Lys Met Glu
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Leu Ser	Gln Pro Glu Val Ser	Glu Asp Phe Glu Glu	Asp Gly Leu
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Gly Val	Leu Pro Ala Phe Thr	Ser Asn Leu Glu Arg	Gly Gly Val
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Glu Lys	Leu Leu Asp Leu Ser	Trp Thr Glu Ser Cys	Lys Pro Thr
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Ala Thr	Glu Pro Leu Phe Lys	Lys Val Ser Pro Trp	Glu Thr Ser
1310	1315	1320	
Thr Ser	Ser Phe Phe Pro Ile	Leu Ala Pro Ala Val	Gly Ser Tyr
1325	1330	1335	
Leu Thr	Pro Thr Thr Arg Ala	His Ser Pro Ala Ser	Leu Ser Phe
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Ala Ser	Tyr Arg Gln Val Ala	Ser Phe Gly Ser Ala	Ala Pro Pro
1355	1360	1365	

Arg Gln Phe Asp Ala Ser Gln Phe Ser Gln Gly Pro Val Pro Gly
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Thr Cys Ala Asp Trp Ile Pro Gln Ser Ala Ser Cys Pro Thr Gly
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Pro Pro Gln Asn Pro Pro Ser Ala Pro Tyr Cys Gly Ile Val Phe
 1400 1405 1410

Ser Gly Ser Ser Leu Ser Ser Ala Gln Ser Ala Pro Leu Gln His
 1415 1420 1425

Pro Gly Gly Phe Thr Thr Arg Pro Ser Ala Gly Thr Phe Pro Glu
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Leu Asp Ser Pro Gln Leu His Phe Ser Leu Pro Thr Asp Pro Asp
 1445 1450 1455

Pro Ile Arg Gly Phe Gly Ser Tyr His Pro Ser Ala Tyr Ser Pro
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Phe His Phe Gln Pro Ser Ala Ala Ser Leu Thr Ala Asn Leu Arg
 1475 1480 1485

Leu Pro Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser Gln Ser
 1490 1495 1500

Arg Thr Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser Val Gly
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Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser Ser
 1520 1525 1530

Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys
 1535 1540 1545

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 1550 1555 1560

Phe Leu Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His
 1565 1570 1575

Trp Gln Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr

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Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu		
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Asn Leu Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly		
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Ile Gln Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu		
1625	1630	1635
Ile Ala Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu		
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Lys Glu Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro		
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Ser Ile Ser Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln		
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Ala Ser Glu Trp Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile		
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Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys		
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<210> 54
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 <212> PRT
 <213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and *Homo sapiens*

<400> 54

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Gly Ile Pro Ala Asn Leu Arg Leu Pro Met Ala Ser Ala Leu Pro Glu
 100 105 110

Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro Val Asp Leu Cys Leu Leu
 115 120 125

Glu Glu Ser Val Gly Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala
 130 135 140

Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln
 145 150 155 160

Asp Ser Cys Phe Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile
 165 170 175

Pro Cys Phe Leu Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln
 180 185 190

His Trp Gln Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr
 195 200 205

Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn

210	215	220
Leu Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln		
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Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr		
	245	250 255
Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile		
	260	265 270
Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn		
	275	280 285
Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg		
	290	295 300
Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu Gly		
305	310	315 320
Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln Pro Ile		
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Ser Thr Val Ser Pro Leu His Arg Val Leu His Tyr Ser Gln Gly		
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 <211> 1056
 <212> DNA
 <213> Artificial Sequence

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 <223> *Saccharomyces cerevisiae* and *Homo sapiens*

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 aaccttaggc tgccaatggc ctctgcttta cctgaggctc tttgcagtca gtcccggact 360
 accccagtag atctctgtct tctagaagaa tcagtaggca gtctcgaagg aagtcgatgt 420

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gaatgggtaa gaagaactga aggacagtac ccatctatct gcccacggct tgaactgggg      960
aacgactggg actctgccac caagcagttg ctgggactcc agcccataag cactgtgtcc     1020
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<210> 56
 <211> 1820
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> *Saccaromyces cerevisiae* and *Homo sapiens*

<400> 56

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
          35           40           45

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Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
          50           55           60

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Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
65           70           75           80

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Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
          85           90           95

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Met Val Met Gly Ile Phe Ala Asn Cys Ile Phe Cys Leu Lys Val Lys

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Asn Gly Gly Lys Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr His Ile		
130	135	140
Ile Leu Asp Asn Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn Ser Ile		
145	150	155
		160
Gln Lys Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser		
165	170	175
Ile Arg Glu Lys Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro Tyr Lys		
180	185	190
Pro Leu Asp Ile Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Ser Glu		
195	200	205
Val Lys Thr Glu Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu Glu Asp		
210	215	220
Thr Val Glu Leu Thr Glu Phe Gly Met Gln Asn Val Glu Ile Pro His		
225	230	235
		240
Leu Pro Gln Asp Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu Lys Val		
245	250	255
Gly Met Glu Gly Gly Gln Glu Ala Val Val Val Glu Leu Gln Cys Ser		
260	265	270
Arg Asp Ser Arg Asp Cys Pro Phe Leu Ile Ser Ser His Phe Leu Leu		
275	280	285
Asp Asp Gly Met Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys Thr Ser		
290	295	300
Glu Asp Ala Ser Glu Tyr Phe Glu Asn Tyr Ile Glu Glu Leu Lys Lys		
305	310	315
		320
Gln Gly Phe Leu Leu Arg Glu His Phe Thr Pro Glu Ala Thr Gln Leu		
325	330	335

Ala Ser Glu Gln Leu Gln Ala Leu Leu Leu Glu Glu Val Met Asn Ser
 340 345 350

Ser Thr Leu Ser Gln Glu Val Ser Asp Leu Val Glu Met Ile Trp Ala
 355 360 365

Glu Ala Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val Asn Arg
 370 375 380

Ile Ser Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu Leu Val
 385 390 395 400

Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln Lys Met
 405 410 415

Met Thr Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met Pro Lys
 420 425 430

Glu Val Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys Gln Leu
 435 440 445

Ile Arg Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys Pro Asn
 450 455 460

Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile Glu His
 465 470 475 480

Val Glu Gln Asn Thr Glu Glu Phe Leu Arg Val Arg Lys Glu Val Leu
 485 490 495

Gln Asn His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile Phe Arg
 500 505 510

Val Gly Arg Val Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu Gly Asn
 515 520 525

Val Arg Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile
 530 535 540

Leu Cys Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val
 545 550 555 560

Gln Arg Thr Asp Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe Ser Asp
 565 570 575

Ser Leu Ser Thr Ser Ile Lys Tyr Ser His Pro Gly Glu Thr Asp Gly
580 585 590

Thr Arg Leu Leu Leu Ile Cys Asp Val Ala Leu Gly Lys Cys Met Asp
595 600 605

Leu His Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp
610 615 620

Ser Val His Gly Val Ser Gln Thr Ala Ser Val Thr Thr Asp Phe Glu
625 630 635 640

Asp Asp Glu Phe Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr
645 650 655

Ile Ile Lys Phe Ser Met Pro Gly Asp Gln Ile Lys Asp Phe His Pro
660 665 670

Ser Asp His Thr Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser Asn Phe
675 680 685

Ser Lys Val Glu Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser Ser Ser
690 695 700

Thr Lys Ala Gly Leu Gln Asp Ala Ser Gly Asn Leu Val Pro Leu Glu
705 710 715 720

Asp Val His Ile Lys Gly Arg Ile Ile Asp Thr Val Ala Gln Val Ile
725 730 735

Val Phe Gln Thr Tyr Thr Asn Lys Ser His Val Pro Ile Glu Ala Lys
740 745 750

Tyr Ile Phe Pro Leu Asp Asp Lys Ala Ala Val Cys Gly Phe Glu Ala
755 760 765

Phe Ile Asn Gly Lys His Ile Val Gly Glu Ile Lys Glu Lys Glu Glu
770 775 780

Ala Gln Gln Glu Tyr Leu Glu Ala Val Thr Gln Gly His Gly Ala Tyr
785 790 795 800

Leu Met Ser Gln Asp Ala Pro Asp Val Phe Thr Val Ser Val Gly Asn

805 810 815
 Leu Pro Pro Lys Ala Lys Val Leu Ile Lys Ile Thr Tyr Ile Thr Glu
 820 825 830
 Leu Ser Ile Leu Gly Thr Val Gly Val Phe Phe Met Pro Ala Thr Val
 835 840 845
 Ala Pro Trp Gln Gln Asp Lys Ala Leu Asn Glu Asn Leu Gln Asp Thr
 850 855 860
 Val Glu Lys Ile Cys Ile Lys Glu Ile Gly Thr Lys Gln Ser Phe Ser
 865 870 875 880
 Leu Thr Met Ser Ile Glu Met Pro Tyr Val Ile Glu Phe Ile Phe Ser
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 Asp Thr His Glu Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala Val Ile
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 915 920 925
 Ile Gly Leu Ser Ala Ala Tyr Leu Pro Arg Met Trp Val Glu Lys His
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 Pro Glu Lys Glu Ser Glu Ala Cys Met Leu Val Phe Gln Pro Asp Leu
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 Asp Val Asp Leu Pro Asp Leu Ala Ser Glu Ser Glu Val Ile Ile Cys
 965 970 975
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 980 985 990
 Gln Ile Thr Leu His Ala Leu Ser Leu Val Gly Glu Lys Gln Lys Val
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 Pro Lys His Ile Thr Ser Asn Thr Thr Ala Ala Glu Phe Ile Met
 1025 1030 1035

Ser Ala Thr Pro Thr Met Gly Asn Thr Asp Phe Trp Lys Thr Leu
 1040 1045 1050

Arg Tyr Leu Ser Leu Leu Tyr Pro Ala Arg Gly Ser Arg Asn Ile
 1055 1060 1065

Leu Leu Val Ser Asp Gly His Leu Gln Asp Glu Ser Leu Thr Leu
 1070 1075 1080

Gln Leu Val Lys Arg Ser Arg Pro His Thr Arg Leu Phe Ala Cys
 1085 1090 1095

Gly Ile Gly Ser Thr Ala Asn Arg His Val Leu Arg Ile Leu Ser
 1100 1105 1110

Gln Cys Gly Ala Gly Val Phe Glu Tyr Phe Asn Ala Lys Ser Lys
 1115 1120 1125

His Ser Trp Arg Lys Gln Ile Glu Asp Gln Met Thr Arg Leu Cys
 1130 1135 1140

Ser Pro Ser Cys His Ser Val Ser Val Lys Trp Gln Gln Leu Asn
 1145 1150 1155

Pro Asp Ala Pro Glu Ala Leu Gln Ala Pro Ala Gln Val Pro Ser
 1160 1165 1170

Leu Phe Arg Asn Asp Arg Leu Leu Val Tyr Gly Phe Ile Pro His
 1175 1180 1185

Cys Thr Gln Ala Thr Leu Cys Ala Leu Ile Gln Glu Lys Glu Phe
 1190 1195 1200

Cys Thr Met Val Ser Thr Thr Glu Leu Gln Lys Thr Thr Gly Thr
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Met Ile His Lys Leu Ala Ala Arg Ala Leu Ile Arg Asp Tyr Glu
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Asp Gly Ile Leu His Glu Asn Glu Thr Ser His Glu Met Lys Lys
 1235 1240 1245

Gln Thr Leu Lys Ser Leu Ile Ile Lys Leu Ser Lys Glu Asn Ser
 1250 1255 1260

Leu Ile Thr Gln Phe Thr Ser Phe Val Ala Val Glu Lys Arg Asp
 1265 1270 1275

Glu Asn Glu Ser Pro Phe Pro Asp Ile Pro Lys Val Ser Glu Leu
 1280 1285 1290

Ile Ala Lys Glu Asp Val Asp Phe Leu Pro Tyr Met Ser Trp Gln
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Gly Glu Pro Gln Glu Ala Val Arg Asn Gln Ser Leu Leu Ala Ser
 1310 1315 1320

Ser Glu Trp Pro Glu Leu Arg Leu Ser Lys Arg Lys His Arg Lys
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Ile Pro Phe Ser Lys Arg Lys Met Glu Leu Ser Gln Pro Glu Val
 1340 1345 1350

Ser Glu Asp Phe Glu Glu Asp Gly Leu Gly Val Leu Pro Ala Phe
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Thr Ser Asn Leu Glu Arg Gly Gly Val Glu Lys Leu Leu Asp Leu
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Ser Trp Thr Glu Ser Cys Lys Pro Thr Ala Thr Glu Pro Leu Phe
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Lys Lys Val Ser Pro Trp Glu Thr Ser Thr Ser Ser Phe Phe Pro
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Ile Leu Ala Pro Ala Val Gly Ser Tyr Leu Thr Pro Thr Thr Arg
 1415 1420 1425

Ala His Ser Pro Ala Ser Leu Ser Phe Ala Ser Tyr Arg Gln Val
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Ala Ser Phe Gly Ser Ala Ala Pro Pro Arg Gln Phe Asp Ala Ser
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Gln Phe Ser Gln Gly Pro Val Pro Gly Thr Cys Ala Asp Trp Ile
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Pro Gln Ser Ala Ser Cys Pro Thr Gly Pro Pro Gln Asn Pro Pro

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Ser Ala Pro Tyr Cys Gly Ile Val Phe Ser Gly Ser Ser Leu Ser		
1490	1495	1500
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Arg Pro Ser Ala Gly Thr Phe Pro Glu Leu Asp Ser Pro Gln Leu		
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His Phe Ser Leu Pro Thr Asp Pro Asp Pro Ile Arg Gly Phe Gly		
1535	1540	1545
Ser Tyr His Pro Ser Ala Tyr Ser Pro Phe His Phe Gln Pro Ser		
1550	1555	1560
Ala Ala Ser Leu Thr Ala Asn Leu Arg Leu Pro Met Ala Ser Ala		
1565	1570	1575
Leu Pro Glu Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro Val Asp		
1580	1585	1590
Leu Cys Leu Leu Glu Glu Ser Val Gly Ser Leu Glu Gly Ser Arg		
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Cys Pro Val Phe Ala Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu		
1610	1615	1620
Leu Ser Glu Val Leu Gln Asp Ser Cys Phe Leu Gln Ile Lys Cys		
1625	1630	1635
Asp Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu Glu Leu Lys Glu		
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Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln Asp Ala Val Pro		
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Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe Trp Lys		
1670	1675	1680
Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn Gly		
1685	1690	1695

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Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr Met Leu Val
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Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile Val Phe
 1730 1735 1740

Lys Ser Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn Ile
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Pro Trp Ala Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg
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Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu
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Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln
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Gln Gly
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 <211> 5463
 <212> DNA
 <213> Artificial Sequence

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 <223> *Saccaromyces cerevisiae* and *Homo sapiens*

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<210> 58
<211> 491
<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

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20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Ala
 225 230 235 240

Asn Leu Arg Leu Pro Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser
 245 250 255

Gln Ser Arg Thr Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser Val
 260 265 270

Gly Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser Ser
 275 280 285

Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys Phe
 290 295 300

Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu
 305 310 315 320

Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln Asp
 325 330 335

Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe
 340 345 350

Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn
 355 360 365

Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln Ser Leu Gly Val
 370 375 380

Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr Met Leu Val Leu
 385 390 395 400

Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile Val Phe Lys Ser
 405 410 415

Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn Ile Pro Trp Ala
 420 425 430

Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg Arg Thr Glu Gly
 435 440 445

Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp
 450 455 460

Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln Pro Ile Ser Thr Val Ser
 465 470 475 480

Pro Leu His Arg Val Leu His Tyr Ser Gln Gly
 485 490

<210> 59
 <211> 1476
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

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 aagctcacc tgaattcat ctgcaccact ggaaagctcc ctgtgccatg gccaacactg 180
 gtcactacct tcacctatgg cgtgcagtgc ttttccagat acccagacca tatgaagcag 240
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 aatagaatcg agctgaaggg cattgacttt aaggaggatg gaaacattct cggccacaag 420
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 gaattaaaag aagaggatga aatagtgtgc acacaacact ggcaggatgc tgtgccttgg 1020
 acagaactcc tcagtctaca gacagaggat ggcttctgga aacttacacc agaactggga 1080

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cagtttattc gcaccaggtt ggaaaaagag ggaatagtgt tcaaatact gatgaaaatg      1260
gatgaccctt ctatttccag gaatattccc tgggcttttg aggcaataaa gcaagcaagt      1320
gaatgggtaa gaagaactga aggacagtac ccatctatct gcccacgggt tgaactgggg      1380
aacgactggg actctgccac caagcagttg ctgggactcc agcccataag cactgtgtcc      1440
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<210> 60

<211> 1961

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 60

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
          20              25              30

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35              40              45

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Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50              55              60

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Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65              70              75              80

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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
          85              90              95

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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100              105              110

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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115              120              125

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Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn

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130

135

140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Met Val
 225 230 235 240

Met Gly Ile Phe Ala Asn Cys Ile Phe Cys Leu Lys Val Lys Tyr Leu
 245 250 255

Pro Gln Gln Gln Lys Lys Lys Leu Gln Thr Asp Ile Lys Glu Asn Gly
 260 265 270

Gly Lys Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr His Ile Ile Leu
 275 280 285

Asp Asn Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn Ser Ile Gln Lys
 290 295 300

Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser Ile Arg
 305 310 315 320

Glu Lys Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro Tyr Lys Pro Leu
 325 330 335

Asp Ile Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Ser Glu Val Lys
 340 345 350

Thr Glu Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu Glu Asp Thr Val
 355 360 365

Glu Leu Thr Glu Phe Gly Met Gln Asn Val Glu Ile Pro His Leu Pro
 370 375 380

Gln Asp Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu Lys Val Gly Met
 385 390 395 400

Glu Gly Gly Gln Glu Ala Val Val Val Glu Leu Gln Cys Ser Arg Asp
 405 410 415

Ser Arg Asp Cys Pro Phe Leu Ile Ser Ser His Phe Leu Leu Asp Asp
 420 425 430

Gly Met Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys Thr Ser Glu Asp
 435 440 445

Ala Ser Glu Tyr Phe Glu Asn Tyr Ile Glu Glu Leu Lys Lys Gln Gly
 450 455 460

Phe Leu Leu Arg Glu His Phe Thr Pro Glu Ala Thr Gln Leu Ala Ser
 465 470 475 480

Glu Gln Leu Gln Ala Leu Leu Leu Glu Glu Val Met Asn Ser Ser Thr
 485 490 495

Leu Ser Gln Glu Val Ser Asp Leu Val Glu Met Ile Trp Ala Glu Ala
 500 505 510

Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val Asn Arg Ile Ser
 515 520 525

Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu Leu Val Lys Ala
 530 535 540

Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln Lys Met Met Thr
 545 550 555 560

Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met Pro Lys Glu Val
 565 570 575

Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys Gln Leu Ile Arg
 580 585 590

Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys Pro Asn Pro Pro
 595 600 605

Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile Glu His Val Glu
610 615 620

Gln Asn Thr Glu Glu Phe Leu Arg Val Arg Lys Glu Val Leu Gln Asn
625 630 635 640

His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile Phe Arg Val Gly
645 650 655

Arg Val Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu Gly Asn Val Arg
660 665 670

Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile Leu Cys
675 680 685

Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val Gln Arg
690 695 700

Thr Asp Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe Ser Asp Ser Leu
705 710 715 720

Ser Thr Ser Ile Lys Tyr Ser His Pro Gly Glu Thr Asp Gly Thr Arg
725 730 735

Leu Leu Leu Ile Cys Asp Val Ala Leu Gly Lys Cys Met Asp Leu His
740 745 750

Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp Ser Val
755 760 765

His Gly Val Ser Gln Thr Ala Ser Val Thr Thr Asp Phe Glu Asp Asp
770 775 780

Glu Phe Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr Ile Ile
785 790 795 800

Lys Phe Ser Met Pro Gly Asp Gln Ile Lys Asp Phe His Pro Ser Asp
805 810 815

His Thr Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser Asn Phe Ser Lys
820 825 830

Val Glu Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser Ser Ser Thr Lys

835	840	845
Ala Gly Leu Gln Asp Ala Ser Gly Asn Leu Val Pro Leu Glu Asp Val		
850	855	860
His Ile Lys Gly Arg Ile Ile Asp Thr Val Ala Gln Val Ile Val Phe		
865	870	875 880
Gln Thr Tyr Thr Asn Lys Ser His Val Pro Ile Glu Ala Lys Tyr Ile		
	885	890 895
Phe Pro Leu Asp Asp Lys Ala Ala Val Cys Gly Phe Glu Ala Phe Ile		
	900	905 910
Asn Gly Lys His Ile Val Gly Glu Ile Lys Glu Lys Glu Glu Ala Gln		
	915	920 925
Gln Glu Tyr Leu Glu Ala Val Thr Gln Gly His Gly Ala Tyr Leu Met		
	930	935 940
Ser Gln Asp Ala Pro Asp Val Phe Thr Val Ser Val Gly Asn Leu Pro		
945	950	955 960
Pro Lys Ala Lys Val Leu Ile Lys Ile Thr Tyr Ile Thr Glu Leu Ser		
	965	970 975
Ile Leu Gly Thr Val Gly Val Phe Phe Met Pro Ala Thr Val Ala Pro		
	980	985 990
Trp Gln Gln Asp Lys Ala Leu Asn Glu Asn Leu Gln Asp Thr Val Glu		
	995	1000 1005
Lys Ile Cys Ile Lys Glu Ile Gly Thr Lys Gln Ser Phe Ser Leu		
	1010	1015 1020
Thr Met Ser Ile Glu Met Pro Tyr Val Ile Glu Phe Ile Phe Ser		
	1025	1030 1035
Asp Thr His Glu Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala Val		
	1040	1045 1050
Ile Ser Thr Met Glu Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser		
	1055	1060 1065

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Val Lys Trp Gln Gln Leu Asn Pro Asp Ala Pro Glu Ala Leu Gln
 1295 1300 1305

 Ala Pro Ala Gln Val Pro Ser Leu Phe Arg Asn Asp Arg Leu Leu
 1310 1315 1320

 Val Tyr Gly Phe Ile Pro His Cys Thr Gln Ala Thr Leu Cys Ala
 1325 1330 1335

 Leu Ile Gln Glu Lys Glu Phe Cys Thr Met Val Ser Thr Thr Glu
 1340 1345 1350

 Leu Gln Lys Thr Thr Gly Thr Met Ile His Lys Leu Ala Ala Arg
 1355 1360 1365

 Ala Leu Ile Arg Asp Tyr Glu Asp Gly Ile Leu His Glu Asn Glu
 1370 1375 1380

 Thr Ser His Glu Met Lys Lys Gln Thr Leu Lys Ser Leu Ile Ile
 1385 1390 1395

 Lys Leu Ser Lys Glu Asn Ser Leu Ile Thr Gln Phe Thr Ser Phe
 1400 1405 1410

 Val Ala Val Glu Lys Arg Asp Glu Asn Glu Ser Pro Phe Pro Asp
 1415 1420 1425

 Ile Pro Lys Val Ser Glu Leu Ile Ala Lys Glu Asp Val Asp Phe
 1430 1435 1440

 Leu Pro Tyr Met Ser Trp Gln Gly Glu Pro Gln Glu Ala Val Arg
 1445 1450 1455

 Asn Gln Ser Leu Leu Ala Ser Ser Glu Trp Pro Glu Leu Arg Leu
 1460 1465 1470

 Ser Lys Arg Lys His Arg Lys Ile Pro Phe Ser Lys Arg Lys Met
 1475 1480 1485

 Glu Leu Ser Gln Pro Glu Val Ser Glu Asp Phe Glu Glu Asp Gly
 1490 1495 1500

 Leu Gly Val Leu Pro Ala Phe Thr Ser Asn Leu Glu Arg Gly Val

1505		1510		1515
Glu Lys Leu Leu Asp Leu Ser Trp Thr Glu Ser Cys Lys Pro Thr				
1520		1525		1530
Ala Thr Glu Pro Leu Phe Lys Lys Val Ser Pro Trp Glu Thr Ser				
1535		1540		1545
Thr Ser Ser Phe Phe Pro Ile Leu Ala Pro Ala Val Gly Ser Tyr				
1550		1555		1560
Leu Thr Pro Thr Thr Arg Ala His Ser Pro Ala Ser Leu Ser Phe				
1565		1570		1575
Ala Ser Tyr Arg Gln Val Ala Ser Phe Gly Ser Ala Ala Pro Pro				
1580		1585		1590
Arg Gln Phe Asp Ala Ser Gln Phe Ser Gln Gly Pro Val Pro Gly				
1595		1600		1605
Thr Cys Ala Asp Trp Ile Pro Gln Ser Ala Ser Cys Pro Thr Gly				
1610		1615		1620
Pro Pro Gln Asn Pro Pro Ser Ala Pro Tyr Cys Gly Ile Val Phe				
1625		1630		1635
Ser Gly Ser Ser Leu Ser Ser Ala Gln Ser Ala Pro Leu Gln His				
1640		1645		1650
Pro Gly Gly Phe Thr Thr Arg Pro Ser Ala Gly Thr Phe Pro Glu				
1655		1660		1665
Leu Asp Ser Pro Gln Leu His Phe Ser Leu Pro Thr Asp Pro Asp				
1670		1675		1680
Pro Ile Arg Gly Phe Gly Ser Tyr His Pro Ser Ala Tyr Ser Pro				
1685		1690		1695
Phe His Phe Gln Pro Ser Ala Ala Ser Leu Thr Ala Asn Leu Arg				
1700		1705		1710
Leu Pro Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser Gln Ser				
1715		1720		1725

Arg Thr Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser Val Gly
 1730 1735 1740

Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser Ser
 1745 1750 1755

Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys
 1760 1765 1770

Phe Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile Pro Cys
 1775 1780 1785

Phe Leu Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His
 1790 1795 1800

Trp Gln Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr
 1805 1810 1815

Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu
 1820 1825 1830

Asn Leu Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly
 1835 1840 1845

Ile Gln Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu
 1850 1855 1860

Ile Ala Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu
 1865 1870 1875

Lys Glu Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro
 1880 1885 1890

Ser Ile Ser Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln
 1895 1900 1905

Ala Ser Glu Trp Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile
 1910 1915 1920

Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys
 1925 1930 1935

Gln Leu Leu Gly Leu Gln Pro Ile Ser Thr Val Ser Pro Leu His
 1940 1945 1950

Arg Val Leu His Tyr Ser Gln Gly
1955 1960

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<211> 5889
<212> DNA
<213> Artificial Sequence

<220>
<223> synthesized and Homo sapiens

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<210> 62
 <211> 385
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens

<400> 62

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Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
          20          25          30

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```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser

```


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Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu		
50	55	60
Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val		
65	70	75
Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe		
85	90	95
Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu		
100	105	110
Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly		
115	120	125
Ile Tyr Gly Ile Pro Ala Asn Leu Arg Leu Pro Met Ala Ser Ala Leu		
130	135	140
Pro Glu Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro Val Asp Leu Cys		
145	150	155
Leu Leu Glu Glu Ser Val Gly Ser Leu Glu Gly Ser Arg Cys Pro Val		
165	170	175
Phe Ala Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu Leu Ser Glu Val		
180	185	190
Leu Gln Asp Ser Cys Phe Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp		
195	200	205
Ser Ile Pro Cys Phe Leu Glu Leu Lys Glu Glu Asp Glu Ile Val Cys		
210	215	220
Thr Gln His Trp Gln Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu		
225	230	235
Gln Thr Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile		
245	250	255
Leu Asn Leu Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly		
260	265	270

Ile Gln Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile
 275 280 285

Ala Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu
 290 295 300

Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro Ser Ile Ser
 305 310 315 320

Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp
 325 330 335

Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu
 340 345 350

Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln
 355 360 365

Pro Ile Ser Thr Val Ser Pro Leu His Arg Val Leu His Tyr Ser Gln
 370 375 380

Gly
 385

<210> 63
 <211> 1158
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens

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 atcaaagtcg aggtgcctaa agtggcaacc cagactgttg gtgggtgtaga gcttctgtga 240
 gccgcatggc gttcgtactt aaatatggaa ctaaccattc caattttcgc tacgaattcc 300
 gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360
 tcagcaatcg cagcaaactc cggcatctac ggaattcctg ccaaccttag gctgccaatg 420
 gcctctgctt tacctgaggc tctttgcagt cagtcccga ctaccccagt agatctctgt 480
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ataaagtgtg atacaaaaga tgacagtatc ccgtgctttc tggaattaaa agaagaggat      660
gaaatagtgt gcacacaaca ctggcaggat gctgtgcctt ggacagaact cctcagtcta      720
cagacagagg atggcttctg gaaacttaca ccagaactgg gacttatatt aaatcttaat      780
acaaatgggt tgcacagctt tcttaaacaa aaaggcattc aatctctagg tgtaaaagga      840
agagaatgtc tcctggacct aattgccaca atgctgggtac tacagtttat tcgcaccagg      900
ttggaaaaag agggaatagt gttcaaata ctgatgaaaa tggatgaccc ttctatttcc      960
aggaatattc cctgggcttt tgaggcaata aagcaagcaa gtgaatgggt aagaagaact     1020
gaaggacagt acccatctat ctgcccacgg cttgaactgg ggaacgactg ggactctgcc     1080
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cattacagtc aaggctaa                                     1158

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<210> 64

<211> 1854

<212> PRT

<213> Artificial Sequence

<220>

<223> Levivirus and Homo sapiens

<400> 64

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Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1           5           10          15

```

```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
          20          25          30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
          35          40          45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
          50          55          60

```

```

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65          70          75          80

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```

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
          85          90          95

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```

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu

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Leu	Lys	Asp	Gly	Asn	Pro	Ile	Pro	Ser	Ala	Ile	Ala	Ala	Asn	Ser	Gly
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Ile	Tyr	Met	Val	Met	Gly	Ile	Phe	Ala	Asn	Cys	Ile	Phe	Cys	Leu	Lys
	130					135					140				
Val	Lys	Tyr	Leu	Pro	Gln	Gln	Gln	Lys	Lys	Lys	Leu	Gln	Thr	Asp	Ile
145					150					155					160
Lys	Glu	Asn	Gly	Gly	Lys	Phe	Ser	Phe	Ser	Leu	Asn	Pro	Gln	Cys	Thr
			165						170					175	
His	Ile	Ile	Leu	Asp	Asn	Ala	Asp	Val	Leu	Ser	Gln	Tyr	Gln	Leu	Asn
			180					185					190		
Ser	Ile	Gln	Lys	Asn	His	Val	His	Ile	Ala	Asn	Pro	Asp	Phe	Ile	Trp
	195						200					205			
Lys	Ser	Ile	Arg	Glu	Lys	Arg	Leu	Leu	Asp	Val	Lys	Asn	Tyr	Asp	Pro
	210					215					220				
Tyr	Lys	Pro	Leu	Asp	Ile	Thr	Pro	Pro	Pro	Asp	Gln	Lys	Ala	Ser	Ser
225					230					235					240
Ser	Glu	Val	Lys	Thr	Glu	Gly	Leu	Cys	Pro	Asp	Ser	Ala	Thr	Glu	Glu
				245					250					255	
Glu	Asp	Thr	Val	Glu	Leu	Thr	Glu	Phe	Gly	Met	Gln	Asn	Val	Glu	Ile
			260					265					270		
Pro	His	Leu	Pro	Gln	Asp	Phe	Glu	Val	Ala	Lys	Tyr	Asn	Thr	Leu	Glu
	275						280					285			
Lys	Val	Gly	Met	Glu	Gly	Gly	Gln	Glu	Ala	Val	Val	Val	Glu	Leu	Gln
	290					295					300				
Cys	Ser	Arg	Asp	Ser	Arg	Asp	Cys	Pro	Phe	Leu	Ile	Ser	Ser	His	Phe
305					310					315					320
Leu	Leu	Asp	Asp	Gly	Met	Glu	Thr	Arg	Arg	Gln	Phe	Ala	Ile	Lys	Lys
				325					330					335	

Thr Ser Glu Asp Ala Ser Glu Tyr Phe Glu Asn Tyr Ile Glu Glu Leu
 340 345 350

Lys Lys Gln Gly Phe Leu Leu Arg Glu His Phe Thr Pro Glu Ala Thr
 355 360 365

Gln Leu Ala Ser Glu Gln Leu Gln Ala Leu Leu Leu Glu Glu Val Met
 370 375 380

Asn Ser Ser Thr Leu Ser Gln Glu Val Ser Asp Leu Val Glu Met Ile
 385 390 395 400

Trp Ala Glu Ala Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val
 405 410 415

Asn Arg Ile Ser Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu
 420 425 430

Leu Val Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln
 435 440 445

Lys Met Met Thr Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met
 450 455 460

Pro Lys Glu Val Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys
 465 470 475 480

Gln Leu Ile Arg Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys
 485 490 495

Pro Asn Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile
 500 505 510

Glu His Val Glu Gln Asn Thr Glu Glu Phe Leu Arg Val Arg Lys Glu
 515 520 525

Val Leu Gln Asn His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile
 530 535 540

Phe Arg Val Gly Arg Val Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu
 545 550 555 560

Gly Asn Val Arg Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val
 565 570 575

Gly Ile Leu Cys Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg
 580 585 590

Gly Val Gln Arg Thr Asp Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe
 595 600 605

Ser Asp Ser Leu Ser Thr Ser Ile Lys Tyr Ser His Pro Gly Glu Thr
 610 615 620

Asp Gly Thr Arg Leu Leu Leu Ile Cys Asp Val Ala Leu Gly Lys Cys
 625 630 635 640

Met Asp Leu His Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly
 645 650 655

Tyr Asp Ser Val His Gly Val Ser Gln Thr Ala Ser Val Thr Thr Asp
 660 665 670

Phe Glu Asp Asp Glu Phe Val Val Tyr Lys Thr Asn Gln Val Lys Met
 675 680 685

Lys Tyr Ile Ile Lys Phe Ser Met Pro Gly Asp Gln Ile Lys Asp Phe
 690 695 700

His Pro Ser Asp His Thr Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser
 705 710 715 720

Asn Phe Ser Lys Val Glu Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser
 725 730 735

Ser Ser Thr Lys Ala Gly Leu Gln Asp Ala Ser Gly Asn Leu Val Pro
 740 745 750

Leu Glu Asp Val His Ile Lys Gly Arg Ile Ile Asp Thr Val Ala Gln
 755 760 765

Val Ile Val Phe Gln Thr Tyr Thr Asn Lys Ser His Val Pro Ile Glu
 770 775 780

Ala Lys Tyr Ile Phe Pro Leu Asp Asp Lys Ala Ala Val Cys Gly Phe
 785 790 795 800

Glu Ala Phe Ile Asn Gly Lys His Ile Val Gly Glu Ile Lys Glu Lys

805

810

815

Glu Glu Ala Gln Gln Glu Tyr Leu Glu Ala Val Thr Gln Gly His Gly
 820 825 830

Ala Tyr Leu Met Ser Gln Asp Ala Pro Asp Val Phe Thr Val Ser Val
 835 840 845

Gly Asn Leu Pro Pro Lys Ala Lys Val Leu Ile Lys Ile Thr Tyr Ile
 850 855 860

Thr Glu Leu Ser Ile Leu Gly Thr Val Gly Val Phe Phe Met Pro Ala
 865 870 875 880

Thr Val Ala Pro Trp Gln Gln Asp Lys Ala Leu Asn Glu Asn Leu Gln
 885 890 895

Asp Thr Val Glu Lys Ile Cys Ile Lys Glu Ile Gly Thr Lys Gln Ser
 900 905 910

Phe Ser Leu Thr Met Ser Ile Glu Met Pro Tyr Val Ile Glu Phe Ile
 915 920 925

Phe Ser Asp Thr His Glu Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala
 930 935 940

Val Ile Ser Thr Met Glu Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser
 945 950 955 960

Leu His Ile Gly Leu Ser Ala Ala Tyr Leu Pro Arg Met Trp Val Glu
 965 970 975

Lys His Pro Glu Lys Glu Ser Glu Ala Cys Met Leu Val Phe Gln Pro
 980 985 990

Asp Leu Asp Val Asp Leu Pro Asp Leu Ala Ser Glu Ser Glu Val Ile
 995 1000 1005

Ile Cys Leu Asp Cys Ser Ser Ser Met Glu Gly Val Thr Phe Leu
 1010 1015 1020

Gln Ala Lys Gln Ile Thr Leu His Ala Leu Ser Leu Val Gly Glu
 1025 1030 1035

Thr Thr Gly Thr Met Ile His Lys Leu Ala Ala Arg Ala Leu Ile
1250 1255 1260

Arg Asp Tyr Glu Asp Gly Ile Leu His Glu Asn Glu Thr Ser His
1265 1270 1275

Glu Met Lys Lys Gln Thr Leu Lys Ser Leu Ile Ile Lys Leu Ser
1280 1285 1290

Lys Glu Asn Ser Leu Ile Thr Gln Phe Thr Ser Phe Val Ala Val
1295 1300 1305

Glu Lys Arg Asp Glu Asn Glu Ser Pro Phe Pro Asp Ile Pro Lys
1310 1315 1320

Val Ser Glu Leu Ile Ala Lys Glu Asp Val Asp Phe Leu Pro Tyr
1325 1330 1335

Met Ser Trp Gln Gly Glu Pro Gln Glu Ala Val Arg Asn Gln Ser
1340 1345 1350

Leu Leu Ala Ser Ser Glu Trp Pro Glu Leu Arg Leu Ser Lys Arg
1355 1360 1365

Lys His Arg Lys Ile Pro Phe Ser Lys Arg Lys Met Glu Leu Ser
1370 1375 1380

Gln Pro Glu Val Ser Glu Asp Phe Glu Glu Asp Gly Leu Gly Val
1385 1390 1395

Leu Pro Ala Phe Thr Ser Asn Leu Glu Arg Gly Gly Val Glu Lys
1400 1405 1410

Leu Leu Asp Leu Ser Trp Thr Glu Ser Cys Lys Pro Thr Ala Thr
1415 1420 1425

Glu Pro Leu Phe Lys Lys Val Ser Pro Trp Glu Thr Ser Thr Ser
1430 1435 1440

Ser Phe Phe Pro Ile Leu Ala Pro Ala Val Gly Ser Tyr Leu Thr
1445 1450 1455

Pro Thr Thr Arg Ala His Ser Pro Ala Ser Leu Ser Phe Ala Ser
1460 1465 1470

Tyr Arg Gln Val Ala Ser Phe Gly Ser Ala Ala Pro Pro Arg Gln

1475		1480		1485
Phe Asp Ala Ser Gln Phe Ser Gln Gly Pro Val Pro Gly Thr Cys				
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Ala Asp Trp Ile Pro Gln Ser Ala Ser Cys Pro Thr Gly Pro Pro				
1505		1510		1515
Gln Asn Pro Pro Ser Ala Pro Tyr Cys Gly Ile Val Phe Ser Gly				
1520		1525		1530
Ser Ser Leu Ser Ser Ala Gln Ser Ala Pro Leu Gln His Pro Gly				
1535		1540		1545
Gly Phe Thr Thr Arg Pro Ser Ala Gly Thr Phe Pro Glu Leu Asp				
1550		1555		1560
Ser Pro Gln Leu His Phe Ser Leu Pro Thr Asp Pro Asp Pro Ile				
1565		1570		1575
Arg Gly Phe Gly Ser Tyr His Pro Ser Ala Tyr Ser Pro Phe His				
1580		1585		1590
Phe Gln Pro Ser Ala Ala Ser Leu Thr Ala Asn Leu Arg Leu Pro				
1595		1600		1605
Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser Gln Ser Arg Thr				
1610		1615		1620
Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser Val Gly Ser Leu				
1625		1630		1635
Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser Ser Asp Thr				
1640		1645		1650
Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys Phe Leu				
1655		1660		1665
Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu				
1670		1675		1680
Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln				
1685		1690		1695

Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp
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Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu
 1715 1720 1725

Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln
 1730 1735 1740

Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala
 1745 1750 1755

Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu
 1760 1765 1770

Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro Ser Ile
 1775 1780 1785

Ser Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln Ala Ser
 1790 1795 1800

Glu Trp Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro
 1805 1810 1815

Arg Leu Glu Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu
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Leu Gly Leu Gln Pro Ile Ser Thr Val Ser Pro Leu His Arg Val
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Leu His Tyr Ser Gln Gly
 1850

<210> 65
 <211> 5565
 <212> DNA
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<220>
 <223> Levivirus and Homo sapiens

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<210> 66
<211> 550
<212> PRT
<213> Photinus pyralis

<400> 66

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Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
35 40 45

Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
100 105 110

Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val
115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
 180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
 195 200 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp
 210 215 220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
 225 230 235 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
 245 250 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
 260 265 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
 275 280 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
 290 295 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
 305 310 315 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
 325 330 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
 340 345 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
 355 360 365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
 405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
 420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
 435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
 465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
 500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
 515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
 530 535 540

Gly Gly Lys Ile Ala Val
 545 550

<210> 67

<211> 1654

<212> DNA

<213> Photinus pyralis

<400> 67

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 aaaaagctcc caatcatcca aaaaattatt atcatggatt ctaaaacgga ttaccaggga 480

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<210> 68

<211> 805

<212> PRT

<213> Artificial Sequence

<220>

<223> Photinus pyralis and Homo sapiens

<400> 68

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Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
20           25           30

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Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
 35 40 45

Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
 50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
 65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
 85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
 100 105 110

Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val
 115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
 130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
 145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
 165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
 180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
 195 200 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp
 210 215 220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
 225 230 235 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
 245 250 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
 260 265 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
 275 280 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
 290 295 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
 305 310 315 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
 325 330 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
 340 345 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
 355 360 365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
 405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
 420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
 435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
 465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu

500

505

510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
 515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
 530 535 540

Gly Gly Lys Ile Ala Val Gly Ile Pro Ala Asn Leu Arg Leu Pro Met
 545 550 555 560

Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro
 565 570 575

Val Asp Leu Cys Leu Leu Glu Glu Ser Val Gly Ser Leu Glu Gly Ser
 580 585 590

Arg Cys Pro Val Phe Ala Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu
 595 600 605

Leu Ser Glu Val Leu Gln Asp Ser Cys Phe Leu Gln Ile Lys Cys Asp
 610 615 620

Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu Glu Leu Lys Glu Glu Asp
 625 630 635 640

Glu Ile Val Cys Thr Gln His Trp Gln Asp Ala Val Pro Trp Thr Glu
 645 650 655

Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu
 660 665 670

Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn Gly Leu His Ser Phe Leu
 675 680 685

Lys Gln Lys Gly Ile Gln Ser Leu Gly Val Lys Gly Arg Glu Cys Leu
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Leu Asp Leu Ile Ala Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg
 705 710 715 720

Leu Glu Lys Glu Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp
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Pro Ser Ile Ser Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln
 740 745 750

Ala Ser Glu Trp Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys
 755 760 765

Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu
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Leu Gly Leu Gln Pro Ile Ser Thr Val Ser Pro Leu His Arg Val Leu
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His Tyr Ser Gln Gly
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 <211> 2418
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Photinus pyralis and Homo sapiens

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<211> 2274

<212> PRT

<213> Artificial Sequence

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<223> Photinus pyralis and Homo sapiens

<400> 70

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 20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
 35 40 45

Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
 50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
 65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
 85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
 100 105 110

Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val
 115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
 130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
 145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
 165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
 180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
 195 200 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp

210

215

220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
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Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
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Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
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Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
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Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
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Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
 305 310 315 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
 325 330 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
 340 345 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
 355 360 365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
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Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
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Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
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Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
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Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
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Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
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Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
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Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
 515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
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Gly Gly Lys Ile Ala Val Met Val Met Gly Ile Phe Ala Asn Cys Ile
 545 550 555 560

Phe Cys Leu Lys Val Lys Tyr Leu Pro Gln Gln Gln Lys Lys Lys Leu
 565 570 575

Gln Thr Asp Ile Lys Glu Asn Gly Gly Lys Phe Ser Phe Ser Leu Asn
 580 585 590

Pro Gln Cys Thr His Ile Ile Leu Asp Asn Ala Asp Val Leu Ser Gln
 595 600 605

Tyr Gln Leu Asn Ser Ile Gln Lys Asn His Val His Ile Ala Asn Pro
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Asp Phe Ile Trp Lys Ser Ile Arg Glu Lys Arg Leu Leu Asp Val Lys
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Asn Tyr Asp Pro Tyr Lys Pro Leu Asp Ile Thr Pro Pro Pro Asp Gln
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Ala Thr Glu Glu Glu Asp Thr Val Glu Leu Thr Glu Phe Gly Met Gln
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Ser Ser His Phe Leu Leu Asp Asp Gly Met Glu Thr Arg Arg Gln Phe
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Leu Lys Pro Val Asn Arg Ile Ser Leu Asn Asp Val Ser Lys Ala Glu
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Gly Ile Leu Leu Leu Val Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala
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Asn Leu Ser Lys Pro Asn Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu

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Gln Asn Ile Val Gly Ile Leu Cys Arg Gly Leu Leu Leu Pro Lys Val		
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Ile Cys Leu Asp Cys Ser Ser Ser Met Glu Gly Val Thr Phe Leu
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Leu Phe Ser Tyr Pro Lys His Ile Thr Ser Asn Thr Thr Ala Ala
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Glu Phe Ile Met Ser Ala Thr Pro Thr Met Gly Asn Thr Asp Phe
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Ser Leu Thr Leu Gln Leu Val Lys Arg Ser Arg Pro His Thr Arg
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Thr Thr Gly Thr Met Ile His Lys Leu Ala Ala Arg Ala Leu Ile				
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Arg Asp Tyr Glu Asp Gly Ile Leu His Glu Asn Glu Thr Ser His				
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Glu Met Lys Lys Gln Thr Leu Lys Ser Leu Ile Ile Lys Leu Ser				
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Lys Glu Asn Ser Leu Ile Thr Gln Phe Thr Ser Phe Val Ala Val				
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Glu Lys Arg Asp Glu Asn Glu Ser Pro Phe Pro Asp Ile Pro Lys				
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1910						1915					1920			
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1925						1930					1935			
Gln	Asn	Pro	Pro	Ser	Ala	Pro	Tyr	Cys	Gly	Ile	Val	Phe	Ser	Gly
1940						1945					1950			
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1985						1990					1995			
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238/429

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520

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Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
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Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 580 585 590

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
 595 600 605

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
 610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 625 630 635 640

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 645 650 655

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 660 665 670

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 675 680 685

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 690 695 700

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
 705 710 715 720

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 725 730 735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
 755 760 765

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 770 775 780

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
 785 790 795 800

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 820 825 830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 835 840 845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 850 855 860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
 865 870 875 880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Arg Gln Ile
 885 890 895

Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
 900 905

<210> 75
 <211> 2730
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo sapiens and Drosophila melanogaster

<400> 75
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 gagagggtac tgtttgcccc catgcgcacg gtgaccgtcc cccacgtca ctactgcaca 180
 gtggccaacc ctgtgtctcg ggatgccag ggcttggtgc tgtttgatgt cacagggcaa 240
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ccaggggagg tgctggaaaa ggacatcaca cccctgcagg tggttctgcc caacactgcc 360
 ctccatctaa aggcgctgct tgattttgag gataaagatg gagacaaggt ggtggcagga 420
 gatgagtggc ttttcgaggg acctggcacg tacatcccc ggaaggaagt ggaggtcgtg 480
 gagatcattc aggccaccat catcaggcag aaccaggctc tgcggctcag gggccgcaag 540
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 cagaacgcac ggatgaagtg gaagaagtga 2730

<210> 76
 <211> 877
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rattus norvegicus and Drosophila melanogaster

<400> 76

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
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His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 50 55 60

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 65 70 75 80

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 225 230 235 240

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 530 535 540

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala

565

570

575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
580 585 590

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met
595 600 605

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
625 630 635 640

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
645 650 655

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
660 665 670

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
675 680 685

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
690 695 700

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
705 710 715 720

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
725 730 735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
740 745 750

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
755 760 765

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
770 775 780

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
785 790 795 800

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cagaacagta	atgtgtcccg	tgtggagggt	ggaccaaaga	cctacatccg	gcaggacaat		120
gagaggggtac	tgtttgcccc	agttcgcacg	gtgaccgtcc	ccccacgcca	ctactgcata		180
gtggccaacc	ctgtgtcccg	ggacaccacg	agttctgtgt	tatttgacat	cacaggacaa		240
gtccgactcc	ggcacgctga	ccaggagatc	cgactagccc	aggaccctt	ccccctgtat		300
ccaggggagg	tgctggaaaa	ggacatcacc	ccactgcagg	tggttctgcc	caacacagca		360
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tactgtgtca	ttcttgacct	aatgggacca	gacggcaaga	accagctggg	acaaaagcgt		900

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 aagcgacaga tcaagatctg gtttcagaac gcacggatga agtgaagaa gtga 2634

<210> 78
 <211> 11
 <212> PRT
 <213> Human immunodeficiency virus type 1

<400> 78

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 1 5 10

<210> 79
 <211> 33
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 79

tacgggcgga agaagcggcg acagaggcga cgg

33

<210> 80
 <211> 904
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Homo sapiens and Human immunodeficiency virus type 1

<400> 80

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
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His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 50 55 60

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 65 70 75 80

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 225 230 235 240

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 435 440 445

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 530 535 540

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His

580

585

590

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
 595 600 605

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
 610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 625 630 635 640

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 645 650 655

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 660 665 670

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 675 680 685

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 690 695 700

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
 705 710 715 720

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 725 730 735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
 755 760 765

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 770 775 780

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
 785 790 795 800

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 820 825 830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 835 840 845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 850 855 860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
 865 870 875 880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Tyr Gly Arg
 885 890 895

Lys Lys Arg Arg Gln Arg Arg Arg
 900

<210> 81
 <211> 2715
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo sapiens and Human immunodeficiency virus type 1

<400> 81
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gaggaggggg aggatgagga gaaggtctca caccaggctg gggaccactg gctcatccgc	1080
ggacccttg agtatgtgcc atctgcaaaa gtggaggtgg tggaggagcg ccaggccatc	1140
cctctagacg agaacgaggg catctatgtg caggatgtca agaccggaaa ggtgcgcgct	1200
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cgcggtcccc acaacgctgc ggtgcaggtg tacgactacc gagagaagcg agccccgctg	1440
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gccatcgaga tcaccaccaa ctcccaggaa gcggcggcca agcatgaggc tcagagactg	2040
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<210> 82
 <211> 872
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rattus norvegicus and Human immunodeficiency virus type 1
 <400> 82

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
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His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 50 55 60

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 65 70 75 80

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 225 230 235 240

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 530 535 540

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 580 585 590

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met
 595 600 605

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
 610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val

263/429

Lys Lys Arg Arg Gln Arg Arg Arg
865 870

<210> 83
<211> 2619
<212> DNA
<213> Artificial Sequence

<220>
<223> Rattus norvegicus and Human immunodeficiency virus type 1

<400> 83
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cgagtaaaga aagtacgaga gatggaactg atctatgccc gggcccagtt ggagctggag 2340
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ctcttcagca cagccttcgg gttgctgggg ctggggtctg atggtcagcc gccagcacag 2580
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```

<210> 84

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> completely synthesized

<400> 84

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Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
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```

```

Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe

```

```
<210> 85
<211> 747
<212> DNA
<213> Artificial Sequence
```

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atgtcctgca gagccggtga aagtgttgat atttttggcg ttgggttttt gactcgttac      120
cagcagaaac caggacagcc acccaaactc ctcattctatc gtgcatccaa cctagaatct      180
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```

gggatccctg tcaggttcag tggcactggg tctaggacag acttcaccct catcattgat      240
cctgtggagg ctgatgatgt tgccacctat tactgtcagc aaactaatga ggatccgtac      300
acgttcggag gggggaccaa gctggaaata aaaggcagta ctagcggcgg tggctccggg      360
ggcggttccg gtggggggcg cagcagcgag gttcagctac aacagtctgg ggcagagctt      420
gtggagccag gggcctcagt caagttgtcc tgcacagctt ctggcttcaa cattaaagac      480
acctatatgc actgggtgaa gcagaggcct gaacagggcc tggaatggat tggaaggatt      540
gatcctgcga atggtaatag taaatatgtc ccgaagttcc agggcaaggc cactataaca      600
gcagacacat cttccaacac agcctacctg cagctcacca gcctgacatc tgaggacact      660
gccgtctatt attgtgtctc gtttggttac tacgtgtctg actatgctat ggcctactgg      720
ggtcaaggaa cctcagtcac cgtctcg                                           747

```

<210> 86

<211> 1072

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 86

```

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1           5           10           15

```

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
20           25           30

```

```

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
35           40           45

```

```

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
50           55           60

```

```

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
65           70           75           80

```

```

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
85           90           95

```

```

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
100          105          110

```

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 225 230 235 240

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 435 440 445

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 530 535 540

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His

580 585 590

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
595 600 605

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
625 630 635 640

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
645 650 655

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
660 665 670

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
675 680 685

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
690 695 700

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
705 710 715 720

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
725 730 735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
740 745 750

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
755 760 765

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
770 775 780

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
785 790 795 800

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 820 825 830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 835 840 845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 850 855 860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
 865 870 875 880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Asp Ile Val
 885 890 895

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
 900 905 910

Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly
 915 920 925

Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
 930 935 940

Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe Ser
 945 950 955 960

Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val Glu
 965 970 975

Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro
 980 985 990

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser
 995 1000 1005

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu
 1010 1015 1020

Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala
 1025 1030 1035

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp
 1040 1045 1050

Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu
 1055 1060 1065

Trp Ile Gly Arg
 1070

<210> 87
 <211> 3429
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens

<400> 87
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aaatatgtcc cgaagttcca gggcaaggcc actataacag cagacacatc ttccaacaca 3300
gcctacctgc agctcaccag cctgacatct gaggacactg ccgtctatta ttgtgctccg 3360
tttggttact acgtgtctga ctatgctatg gcctactggg gtcaaggaac ctcagtcacc 3420
gtctcgtga 3429

```

<210> 88
 <211> 1040
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 88

```

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1           5           10           15

```

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
20           25           30

```

```

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
35           40           45

```

```

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
50           55           60

```

```

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
65           70           75           80

```

```

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
85           90           95

```

```

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
100          105          110

```

```

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp

```

115

120

125

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 225 230 235 240

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 530 535 540

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 580 585 590

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met
 595 600 605

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
 610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 625 630 635 640

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 645 650 655

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 660 665 670

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 675 680 685

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 690 695 700

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
 705 710 715 720

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 725 730 735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
 755 760 765

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 770 775 780

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 785 790 795 800

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile

820

825

830

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
 835 840 845

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Asp Ile Val
 850 855 860

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
 865 870 875 880

Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly
 885 890 895

Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
 900 905 910

Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe Ser
 915 920 925

Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val Glu
 930 935 940

Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro
 945 950 955 960

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser
 965 970 975

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Val
 980 985 990

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val
 995 1000 1005

Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
 1010 1015 1020

Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 1025 1030 1035

Gly Arg
 1040

<210> 89
 <211> 3333
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus

<400> 89
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 gagagggtac tgtttgcccc agttcgcacg gtgaccgtcc cccacgcca ctactgcata 180
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 ctgcatctta aggcgttgct ggactttgag gataagaatg gagacaaggt catggcagga 420
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 gagtgccttg accgggaggg caaggggccc gtgacaggtg aggagtggct ggtccgatcc 600
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 gtgctccacc gcaccgggga ggaatggta gtgacagtgc aggacacaga agcccatggt 780
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 gtgattggaa gcacctacat gctgactcag gatgaagtcc tgtgggaaaa ggagctgcct 1260
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actgccgtct attattgtgc tccgtttggt tactacgtgt ctgactatgc tatggcctac 3300
 tgggggtcaag gaacctcagt caccgtctcg tga 3333

<210> 90
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 90

Met Gly Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys
 1 5 10 15

Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala
 20 25 30

Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp
 35 40 45

Leu Lys Trp Trp Glu Leu Arg Ala
 50 55

<210> 91
 <211> 171
 <212> DNA
 <213> Homo sapiens

<400> 91
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 gtttgatatgt atatcgaagc tctggacaaa tatgcttgca actgtgttgt tggttacatc 120
 ggtgagcggt gccagtatcg cgacctgaaa tgggtgggaac tgcgtgcatg a 171

<210> 92
 <211> 949
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized from two Homo sapiens sequences

<400> 92

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 1 5 10 15

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 50 55 60

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 65 70 75 80

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 225 230 235 240

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 435 440 445

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg

284/429

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
740 745 750

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
755 760 765

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
770 775 780

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
785 790 795 800

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
820 825 830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
835 840 845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
850 855 860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
865 870 875 880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Met Gly Asn
885 890 895

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
900 905 910

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
915 920 925

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
930 935 940

Trp Glu Leu Arg Ala
945

<210> 93

<211> 2850

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesized from two Homo sapiens sequences

<400> 93

```

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gagagggtac tgtttgcccc catgcgcacg gtgaccgtcc cccacgtca ctactgcaca    180
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gagatcattc aggccaccat catcaggcag aaccaggctc tgcggctcag ggcccgaag    540
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gtaggggcgt acctcccagc ggtgtttgag gaggttctgg atttggtgga cgccgtcatc    660
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<210> 94

<211> 917

<212> PRT

<213> Artificial Sequence

<220>

<223> Rattus norvegicus and Homo sapiens

<400> 94

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His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 50 55 60

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 65 70 75 80

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 115 120 125

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 145 150 155 160

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 165 170 175

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 210 215 220

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 225 230 235 240

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 245 250 255

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 260 265 270

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 340 345 350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr

485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
530 535 540

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys
545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
580 585 590

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met
595 600 605

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
625 630 635 640

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
645 650 655

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
660 665 670

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
675 680 685

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
690 695 700

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
705 710 715 720

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 725 730 735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
 755 760 765

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 770 775 780

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 785 790 795 800

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 820 825 830

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
 835 840 845

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Met Gly Asn
 850 855 860

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
 865 870 875 880

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
 885 890 895

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
 900 905 910

Trp Glu Leu Arg Ala
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<210> 95

<211> 2754

<212> DNA

<213> Artificial Sequence

<220>

<223> Rattus norvegicus and Homo sapiens

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 ctgcatctta aggcgttgct ggactttgag gataagaatg gagacaaggt catggcagga 420
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 tctgccgggc gacccaagcg tctcatgcc cgccgtgcac tctgcctact gctgggacct 1560
 gatttcttta ctgatgtcat caccatcgaa actgcagatc atgccagggt gcagctgcag 1620
 cttgcctaca actggcactt tgaactgaag aaccggaatg acctgcaga ggcagccaag 1680


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atggctgttt ttggctttga gatgtctgaa gacacaggtc ctgatggcac actcctgccc 1860
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cagtcagtgg agcccgtgga ccagaggacc cgggatgccc ttcagcgcag cgttcagctg 1980
gccatcgaaa ttaccacca ctcccaggag gcagcagcca agcacgaggc tcagagactg 2040
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cgagtaaaga aagtacgaga gatggaactg atctatgccc gggcccagtt ggagctggag 2340
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aagatgggta actctgactc cgaatgcccg ctgtctcacg acggttattg cctgcatgat 2640
gggtgtttgta tgtatatcga agctctggac aaatatgctt gcaactgtgt tgttggttac 2700
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<210> 96

<211> 1005

<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and *Homo sapiens* and *Drosophila melanogaster*

<400> 96

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Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
1           5           10           15

```

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20           25           30

```

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35           40           45

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Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr

275

280

285

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 325 330 335

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 355 360 365

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 435 440 445

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 515 520 525

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 530 535 540

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 545 550 555 560

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 565 570 575

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 625 630 635 640

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
 645 650 655

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
 690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
 805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
 850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
 885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
 965 970 975

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Arg Gln Ile

980

985

990

Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
 995 1000 1005

<210> 97
 <211> 3018
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Saccharomyces cerevisiae* and *Homo sapiens* and *Drosophila melanogaster*

<400> 97
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 gagttcatca tccgcatccc cccataccac tatatccatg tgctggacca gaacagcaac 360
 gtgtcccgtg tggaggtcgg gccaaagacc tacatccggc aggacaatga gagggctactg 420
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 gtgtctcggg atgccaggg cttggtgctg tttgatgtca cagggcaagt tcggcttcgc 540
 cacgctgacc tcgagatccg gctggcccag gaccccttcc ccctgtaccc aggggaggtg 600
 ctggaaaagg acatcacacc cctgcaggtg gttctgcca aactgcccct ccatctaaag 660
 gcgctgcttg attttgagga taaagatgga gacaaggtgg tggcaggaga tgagtggctt 720
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 gagaagtctt ttttctcca gccaggagag cagctggaac aaggcatcca ggatgtgtat 1260

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3018

atgaagtgga agaagtga

<210> 98
<211> 973
<212> PRT
<213> Artificial Sequence

<220>
<223> *Saccaromyces cerevisiae* and *Rattus norvegicus* and *Drosophila melanogaster*

<400> 98

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 355 360 365

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 435 440 445

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 515 520 525

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 530 535 540

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 545 550 555 560

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 565 570 575

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 625 630 635 640

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys

645

650

655

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met
 690 695 700

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
 805 810 815

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
 850 855 860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 865 870 875 880

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Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
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Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
 930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Arg Gln Ile
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Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
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 <211> 2922
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Saccaromyces cerevisiae* and *Rattus norvegicus* and *Drosophila melanogaster*

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gaactcttgg agcttgaggc tatgagcatg gctgtggaga gcacgggtaa tgccaaagca	2460

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<210> 100
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 <213> Artificial Sequence

<220>
 <223> synthesized and *Saccharomyces cerevisiae* and *Homo sapiens*

<400> 100

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
 325 330 335

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
 355 360 365

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln
 435 440 445

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 515 520 525

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 530 535 540

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 545 550 555 560

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 565 570 575

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg

595

600

605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 625 630 635 640

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
 645 650 655

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
 690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
 805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
 850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
 885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
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Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Asp Ile Val
 980 985 990

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
 995 1000 1005

Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val
 1010 1015 1020

Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys
 1025 1030 1035

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
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Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile
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Asp Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln
 1070 1075 1080

Thr Asn Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
 1085 1090 1095

Ile Lys Gly Ser Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
 1100 1105 1110

Gly Gly Gly Ser Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu
 1115 1120 1125

Leu Val Glu Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser
 1130 1135 1140

Gly Phe Asn Ile Lys Asp Thr Tyr Met His Trp Val Lys Gln Arg
 1145 1150 1155

Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn
 1160 1165 1170

Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys Ala Thr Ile
 1175 1180 1185

Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu Thr Ser
 1190 1195 1200

Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly
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Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr
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Ser Val Thr Val Ser
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<210> 101

<211> 3717

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and *Saccharomyces cerevisiae* and *Homo sapiens*

<400> 101

WO 2004/081533

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<210> 102
 <211> 1206
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and *Saccaromyces cerevisiae* and *Rattus norvegicus*

<400> 102

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 355 360 365

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 435 440 445

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 515 520 525

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 530 535 540

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 545 550 555 560

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 565 570 575

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn

625	630	635	640
Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys	645	650	655
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala	660	665	670
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His	675	680	685
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met	690	695	700
Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp	705	710	715
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val	725	730	735
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg	740	745	750
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala	755	760	765
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu	770	775	780
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys	785	790	795
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly	805	810	815
Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu	820	825	830
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala	835	840	845
Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met	850	855	860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
 885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
 930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Asp Ile Val
 945 950 955 960

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
 965 970 975

Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly
 980 985 990

Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
 995 1000 1005

Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe
 1010 1015 1020

Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro
 1025 1030 1035

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
 1040 1045 1050

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 1055 1060 1065

Gly Ser Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 1070 1075 1080

Gly Ser Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val
 1085 1090 1095

Glu Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe
1100 1105 1110

Asn Ile Lys Asp Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu
1115 1120 1125

Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn
1130 1135 1140

Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala
1145 1150 1155

Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu Thr Ser Leu Thr
1160 1165 1170

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr
1175 1180 1185

Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr Ser Val
1190 1195 1200

Thr Val Ser
1205

<210> 103
<211> 3621
<212> DNA
<213> Artificial Sequence

<220>
<223> synthesized and *Saccharomyces cerevisiae* and *Rattus norvegicus*

<400> 103
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tctcccaaaa ccaaaaggct tccgctgact agggcacatc tgacagaagt ggaatcaagg 180
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gaggccatca tccgcatccc cccataccac tacatccatg tgctggacca gaacagtaat 360
gtgtcccggtg tggagggttg accaaagacc tacatccggc aggacaatga gaggggtactg 420
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gtgtccccggg acaccagag ttctgtgtta ttgacatca caggacaagt ccgactccgg 540
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ggctttgaga tgtctgaaga cacaggtcct gatggcacac tcctgcccga ggctcgagac 2160
caggcagtct tccccaaaa cgggctggta gtcagcagtg tggatgtgca gtcagtggag 2220

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aatggtaata gtaaatatgt cccgaagttc cagggcaagg ccactataac agcagacaca 3480
tcttccaaca cagcctacct gcagctcacc agcctgacat ctgaggacac tgccgtctat 3540
tattgtgctc cgtttggtta ctacgtgtct gactatgcta tggcctactg gggtaagga 3600
acctcagtca ccgtctcgtg a 3621

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<210> 104

<211> 1045

<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and two *Homo sapiens* sequences

<400> 104

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
225 230 235 240

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu

465 470 475 480
 Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495
 Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510
 Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 515 520 525
 Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
 530 535 540
 Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
 545 550 555 560
 Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
 565 570 575
 Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 580 585 590
 Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605
 Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620
 Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 625 630 635 640
 Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
 645 650 655
 Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 660 665 670
 Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685
 Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
 690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
 805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
 850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
 865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
 885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
 915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
 930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
 945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
 965 970 975

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Met Gly Asn
 980 985 990

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
 995 1000 1005

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
 1010 1015 1020

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu
 1025 1030 1035

Lys Trp Trp Glu Leu Arg Ala
 1040 1045

<210> 105
 <211> 3138
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> *Saccaromyces cerevisiae* and two *Homo sapiens* sequences

<400> 105
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 ctagaaagac tggaacagct atttctactg atttttctctc gagaagacct tgacatgatt 240
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 gtgtcccggtg tggaggctcg gccaagacc tacatccggc aggacaatga gaggggtactg 420
 tttgccccca tgcgcatggg gaccgtcccc ccacgtcact actgcacagt ggccaaccct 480
 gtgtctcggg atgcccaggg cttggtgctg tttgatgtca cagggcaagt tcggcttcgc 540
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ctggaaaagg acatcacacc cctgcagggtg gttctgcccc acactgccct ccatctaaag	660
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 cacgacgggt attgcctgca tgatggtgtt tgtatgtata tcgaagctct ggacaaatat 3060
 gcttgcaact gtgttgttgg ttacatcggt ggcggttgc agtatcgca cctgaaatgg 3120
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<210> 106

<211> 1013

<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccharomyces cerevisiae* and *Rattus norvegicus* and *Homo sapiens*

<400> 106

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
 340 345 350

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
 355 360 365

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
 435 440 445

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp
 515 520 525

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro
 530 535 540

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His

545	550	555	560
Asn Ala Ala Val	Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val		
565	570	575	
Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr			
580	585	590	
Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg			
595	600	605	
Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr			
610	615	620	
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn			
625	630	635	640
Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys			
645	650	655	
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala			
660	665	670	
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His			
675	680	685	
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met			
690	695	700	
Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp			
705	710	715	720
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val			
725	730	735	
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg			
740	745	750	
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala			
755	760	765	
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu			
770	775	780	

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
805 810 815

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
835 840 845

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
850 855 860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Met Gly Asn
945 950 955 960

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
965 970 975

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
980 985 990

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
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Trp Glu Leu Arg Ala
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<210> 107
 <211> 3042
 <212> DNA
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<220>

<223> *Saccaromyces cerevisiae* and *Rattus norvegicus* and *Homo sapiens*

<400> 107

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<210> 108
<211> 1000
<212> PRT

<213> Artificial Sequence

<220>

<223> Saccaromyces cerevisiae and Homo sapiens and Human immunodeficiency virus type 1

<400> 108

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35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu
225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val
245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu
260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr
275 280 285

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val
290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
305 310 315 320

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly
325 330 335

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr
340 345 350

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro
355 360 365

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val
370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile
405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala
420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln

435

440

445

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
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Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu
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Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu
 500 505 510

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp
 515 520 525

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro
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Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His
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Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val
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Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
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Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys
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Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
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Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr
690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp
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Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly
805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu
850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu
885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
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Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu
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Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser
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Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro
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Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Tyr Gly Arg
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Lys Lys Arg Arg Gln Arg Arg Arg
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<210> 109

<211> 3003

<212> DNA

<213> Artificial Sequence

<220>

<223> *Saccharomyces cerevisiae* and *Homo sapiens* and Human
 immunodeficiency virus type 1

<400> 109

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 <211> 968
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> *Saccaromyces cerevisiae* and *Rattus norvegicus* and Human immunodeficiency virus type 1

<400> 110

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly
 325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr

340 345 350
 Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro
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 Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met
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 Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly
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 Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile
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 Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala
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 Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln
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 Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser
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 Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln
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 Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val
 565 570 575

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn
 625 630 635 640

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys
 645 650 655

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met
 690 695 700

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly
 805 810 815

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala
835 840 845

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met
850 855 860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala
865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu
885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile
915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu
930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Tyr Gly Arg
945 950 955 960

Lys Lys Arg Arg Gln Arg Arg Arg
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<210> 111

<211> 2907

<212> DNA

<213> Artificial Sequence

<220>

<223> *Saccharomyces cerevisiae* and *Rattus norvegicus* and Human
immunodeficiency virus type 1

<400> 111

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<210> 112
<211> 1040
<212> PRT
<213> Artificial Sequence

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<220>
<223> Levivirus and Homo sapiens and Drosophila melanogaster

```

```

<400> 112

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```

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1           5           10           15

```

```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20           25           30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35           40           45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
50           55           60

```

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr
130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
165 170 175

Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val
180 185 190

Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val
195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala
210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
245 250 255

Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp
260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val
275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala
290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu
305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu
325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp
355 360 365

Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val
370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly
385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu
405 410 415

Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu
435 440 445

Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
450 455 460

Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val
465 470 475 480

Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr
485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
500 505 510

Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val

350/429

Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala
 770 775 780

Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln
 785 790 795 800

Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg
 805 810 815

Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys
 820 825 830

Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu
 835 840 845

Ser Thr Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala
 850 855 860

Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln
 865 870 875 880

Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val
 885 890 895

Arg Glu Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val
 900 905 910

Ser Lys Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln
 915 920 925

Met Thr Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala
 930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
 945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala
 965 970 975

Phe Gly Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg
 980 985 990

Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala
 995 1000 1005

Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu
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Arg Arg Gln Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp
 1025 1030 1035

Lys Lys
 1040

<210> 113
 <211> 3123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens and Drosophila melanogaster

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 gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360
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gttgtgcccc	tcaccaccct	gggccccac	aactactgcg	tgattctcga	ccctgtcggg	1260
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tga 3123

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<210> 114
<211> 1008
<212> PRT
<213> Artificial Sequence

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<220>
<223> Levivirus and Rattus norvegicus and Drosophila melanogaster

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<400> 114

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Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1          5          10          15

```

```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20          25          30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35          40          45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
50          55          60

```

```

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65          70          75          80

```

```

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85          90          95

```

```

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100         105         110

```

```

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Asn Ser Gly
115         120         125

```

```

Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr
130         135         140

```

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
 145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
 165 170 175

Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val
 180 185 190

Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile
 195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala
 210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
 225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
 245 250 255

Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp
 260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
 500 505 510

Leu Asp Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val
 530 535 540

Leu Trp Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu
 545 550 555 560

Gly His Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro
 565 570 575

Leu Gln Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg
 580 585 590

Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg
 595 600 605

Ala Arg Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu

610

615

620

Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His
 625 630 635 640

Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp
 645 650 655

Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu
 660 665 670

Ala Tyr Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu
 675 680 685

Ala Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys
 690 695 700

Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp
 705 710 715 720

Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly
 725 730 735

Phe Glu Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys
 740 745 750

Ala Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser
 755 760 765

Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala
 770 775 780

Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln
 785 790 795 800

Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg
 805 810 815

Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys
 820 825 830

Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu
 835 840 845

Ser Thr Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala
850 855 860

Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln
865 870 875 880

Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val
885 890 895

Arg Glu Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val
900 905 910

Ser Lys Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu
915 920 925

Met Thr Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala
930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala
965 970 975

Phe Gly Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
980 985 990

Arg Gln Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
995 1000 1005

<210> 115
<211> 3027
<212> DNA
<213> Artificial Sequence

<220>
<223> Levivirus and Rattus norvegicus and Drosophila melanogaster

<400> 115
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<210> 116
<211> 1273
<212> PRT
<213> Artificial Sequence

<220>
<223> Levivirus and Homo sapiens and synthesized

<400> 116

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu

50 55 60
 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 65 70 75 80
 Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95
 Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110
 Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125
 Ile Tyr Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr
 130 135 140
 His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
 145 150 155 160
 Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
 165 170 175
 Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val
 180 185 190
 Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val
 195 200 205
 Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala
 210 215 220
 Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
 225 230 235 240
 Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
 245 250 255
 Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp
 260 265 270
 Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp
 355 360 365

Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu
 405 410 415

Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu
 435 440 445

Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
 450 455 460

Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
 500 505 510

Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val
 530 535 540

Leu Trp Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys
 545 550 555 560

Gly Gln Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser
 565 570 575

Leu Gln Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg
 580 585 590

Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg
 595 600 605

Ala Arg Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu
 610 615 620

Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His
 625 630 635 640

Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp
 645 650 655

Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu
 660 665 670

Ala Tyr Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu
 675 680 685

Thr Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys
 690 695 700

Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp
 705 710 715 720

Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly
 725 730 735

Phe Glu Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg
 740 745 750

Pro Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser

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Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala
 995 1000 1005

Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu
 1010 1015 1020

Arg Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser
 1025 1030 1035

Leu Gly Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val
 1040 1045 1050

Asp Ile Phe Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro
 1055 1060 1065

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu
 1070 1075 1080

Ser Gly Ile Pro Val Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp
 1085 1090 1095

Phe Thr Leu Ile Ile Asp Pro Val Glu Ala Asp Asp Val Ala Thr
 1100 1105 1110

Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro Tyr Thr Phe Gly Gly
 1115 1120 1125

Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Gly Gly Ser
 1130 1135 1140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Val Gln Leu Gln
 1145 1150 1155

Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys Leu
 1160 1165 1170

Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His
 1175 1180 1185

Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg
 1190 1195 1200

Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln
 1205 1210 1215

Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
 1220 1225 1230

Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr
 1235 1240 1245

Cys Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr
 1250 1255 1260

Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 1265 1270

<210> 117
 <211> 3822
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Levivirus and Homo sapiens and synthesized

<400> 117
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 caggcttaca aagtaacctg tagcggttcgt cagagctctg cgcagaatcg caaatacacc 180
 atcaaagtcg aggtgcctaa agtggcaacc cagactgttg gtggtgtaga gttcctgtga 240
 gccgcatggc gtctgtactt aaatatggaa ctaaccattc caattttcgc tacgaattcc 300
 gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360
 tcagcaatcg cagcaaatc cggcatctac cccatggcaa ctgaagagtt catcatccgc 420
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 atggtgaccg tccccccacg tcactactgc acagtggcca accctgtgtc tcgggatgcc 600
 cagggtcttg tgctgtttga tgtcacaggg caagttcggc ttcgccacgc tgacctcgag 660
 atccggcttg cccaggaccc cttccccctg taccagggg aggtgctgga aaaggacatc 720
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<210> 118
 <211> 1241
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Levivirus and Rattus norvegicus and synthesized

<400> 118

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
 1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser

35

40

45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr
130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
165 170 175

Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val
180 185 190

Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile
195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala
210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
245 250 255

Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp
260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val
275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala
290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly
305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu
325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp
355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val
370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly
385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu
405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu
435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val
465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr
485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro
500 505 510

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<210> 126
 <211> 1003
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Levivirus and Rattus norvegicus and Human immunodeficiency virus
 type 1

<400> 126

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
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Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr
 130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu
 145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe
 165 170 175

Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val
 180 185 190

Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile
 195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala
 210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile
 225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala
 245 250 255

Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp
 260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val
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Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly
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Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro

500

505

510

Leu Asp Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys
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Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val
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Leu Trp Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu
 545 550 555 560

Gly His Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro
 565 570 575

Leu Gln Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg
 580 585 590

Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg
 595 600 605

Ala Arg Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu
 610 615 620

Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His
 625 630 635 640

Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp
 645 650 655

Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu
 660 665 670

Ala Tyr Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu
 675 680 685

Ala Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys
 690 695 700

Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp
 705 710 715 720

Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly
 725 730 735

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Phe Glu Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys
 740 745 750

Ala Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser
 755 760 765

Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala
 770 775 780

Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln
 785 790 795 800

Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg
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Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys
 820 825 830

Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu
 835 840 845

Ser Thr Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala
 850 855 860

Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln
 865 870 875 880

Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val
 885 890 895

Arg Glu Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val
 900 905 910

Ser Lys Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu
 915 920 925

Met Thr Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala
 930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser
 945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala
 965 970 975

Phe Gly Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys
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Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 995 1000

<210> 127

<211> 3012

<212> DNA

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus and Human immunodeficiency virus
 type 1

<400> 127

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 aggcgacggt ga 3012

<210> 128
 <211> 926
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens and Drosophila melanogaster

<400> 128

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 20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu
 610 615 620

Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp

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Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala
 885 890 895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Arg Gln
 900 905 910

Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
 915 920 925

<210> 129

<211> 2781

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens and Drosophila melanogaster

<400> 129

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<211> 894
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus and Drosophila melanogaster

<400> 130

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
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 20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val

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Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Tyr Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala
675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg
690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg
705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr
725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile
740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu
770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr
805 810 815

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
835 840 845

Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly
850 855 860

Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Arg Gln
865 870 875 880

Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
885 890

<210> 131

<211> 2685

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Rattus norvegicus and Drosophila melanogaster

<400> 131

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aagccccttc agccctcagc tccaaggaac aagaccgag tggtcagcta ccgtgtccccg     1440
cacaatgcag cgggtgcaggt ctatgactac agagccaaga gagcccgtgt ggtctttggg     1500

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<210> 132

<211> 1159

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 132

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Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr
          20          25          30

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Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe

500

505

510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
545 550 555 560

Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala
565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu
610 615 620

Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg
625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp
645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln
660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala
675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg
690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg
705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr
725 730 735

Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile
 740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu
 770 775 780

Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
 785 790 795 800

Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr
 805 810 815

Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
 835 840 845

Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala
 865 870 875 880

Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala
 885 890 895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Asp Ile
 900 905 910

Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
 915 920 925

Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val
 930 935 940

Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
 945 950 955 960

Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe
 965 970 975

Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val
 980 985 990

Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp
 995 1000 1005

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser
 1010 1015 1020

Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1025 1030 1035

Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro
 1040 1045 1050

Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
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Lys Asp Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly
 1070 1075 1080

Leu Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys
 1085 1090 1095

Tyr Val Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr
 1100 1105 1110

Ser Ser Asn Thr Ala Tyr Leu Gln Leu Thr Ser Leu Thr Ser Glu
 1115 1120 1125

Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr Val Ser
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Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
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 <212> DNA
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<220>

<223> synthesized and Homo sapiens

<400> 133

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ctgtttgccc ccatcgcat ggtgacgctc cccccacgctc actactgcac agtggccaac      240
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 <211> 1127
 <212> PRT
 <213> Artificial Sequence

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 <223> synthesized and Rattus norvegicus

<400> 134

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Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg
 245 250 255

Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp

645	650	655
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Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala 675 680 685		
Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg 690 695 700		
Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg 705 710 715 720		
Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr 725 730 735		
Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile 740 745 750		
Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu 755 760 765		
Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu 770 775 780		
Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys 785 790 795 800		
Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr 805 810 815		
Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro 820 825 830		
Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu 835 840 845		
Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly 850 855 860		
Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Asp Ile 865 870 875 880		

Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
885 890 895

Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val
900 905 910

Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
915 920 925

Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe
930 935 940

Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val
945 950 955 960

Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp
965 970 975

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr
980 985 990

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu
995 1000 1005

Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala
1010 1015 1020

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp
1025 1030 1035

Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu
1040 1045 1050

Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val
1055 1060 1065

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser
1070 1075 1080

Asn Thr Ala Tyr Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr
1085 1090 1095

Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr
1100 1105 1110

Ala Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
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<220>
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```

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<210> 136
 <211> 966
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and two Homo sapiens sequences

<400> 136

```

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1          5          10          15

```

```

Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr
          20          25          30

```

```

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
          35          40          45

```

```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
          50          55          60

```

```

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
65          70          75          80

```

```

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
          85          90          95

```

```

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
          100          105          110

```

```

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
          115          120          125

```

```

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
          130          135          140

```

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu

610	615	620
Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg		
625	630	635 640
Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp		
	645	650 655
Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln		
	660	665 670
Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala		
	675	680 685
Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg		
	690	695 700
Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg		
705	710	715 720
Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr		
	725	730 735
Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile		
	740	745 750
Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu		
	755	760 765
Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu		
	770	775 780
Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys		
785	790	795 800
Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr		
	805	810 815
Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro		
	820	825 830
Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu		
	835	840 845

Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly
850 855 860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala
865 870 875 880

Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala
885 890 895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Met Gly
900 905 910

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
915 920 925

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
930 935 940

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
945 950 955 960

Trp Trp Glu Leu Arg Ala
965

<210> 137
<211> 2901
<212> DNA
<213> Artificial Sequence

<220>
<223> synthesized and two Homo sapiens sequences

<400> 137
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ctgtttgccc ccatgcgcat ggtgaccgtc cccccacgtc actactgcac agtggccaac 240
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<210> 138

<211> 934

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Rattus norvegicus and Homo sapiens

<400> 138

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
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Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr
 20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp

100 105 110
 Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125
 Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140
 Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp
 145 150 155 160
 Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val
 165 170 175
 Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg
 180 185 190
 Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val
 195 200 205
 Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala
 210 215 220
 Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240
 Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg
 245 250 255
 Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270
 Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val
 275 280 285
 Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro
 290 295 300
 Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320
 Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala
 675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg
 690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg
 705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr
 725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile
 740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu
 770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
 785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr

805

810

815

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
 835 840 845

Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Met Gly
 865 870 875 880

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
 885 890 895

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
 900 905 910

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
 915 920 925

Trp Trp Glu Leu Arg Ala
 930

<210> 139
 <211> 2805
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus and Homo sapiens

<400> 139
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<210> 140

<211> 921

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens and Human immunodeficiency virus
type 1

<400> 140

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Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
35           40           45

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```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
50           55           60

```

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Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
65           70           75           80

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Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
85           90           95

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Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
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Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val
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Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro
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Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
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Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly
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Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg
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Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
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Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
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Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln
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Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln
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Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
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His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg
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Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe
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Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
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Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
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Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
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Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala

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His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu		
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Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp		
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Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln		
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Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala		
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Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg		
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Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg		
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Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile		
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Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu		
755	760	765
Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu		
770	775	780
Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys		
785	790	795
		800

Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr
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Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
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Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala
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Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala
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Arg Lys Lys Arg Arg Gln Arg Arg Arg
 915 920

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 <211> 2766
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthesized and Homo sapiens and Human immunodeficiency virus
 type 1

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthesized and Rattus norvegicus and Human immunodeficiency virus type 1

<400> 142

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 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
 50 55 60

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
 65 70 75 80

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
 130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val
 165 170 175

Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val
 195 200 205

Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg
 245 250 255

Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp
 260 265 270

Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val
 275 280 285

Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro
 290 295 300

Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys

340

345

350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His
 355 360 365

Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp
 385 390 395 400

Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp
 420 425 430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile
580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe
595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu
610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg
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645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln
660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala
675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg
690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg
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Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr
725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile
740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu
755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu
770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys
785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr
805 810 815

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu
 835 840 845

Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly
 850 855 860

Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Tyr Gly
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Arg Lys Lys Arg Arg Gln Arg Arg Arg
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<210> 143

<211> 2670

<212> DNA

<213> Artificial Sequence

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<400> 143

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